GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: November 16, 2004, 16:34:37 ; Search time 40 Seconds
(without alignments)
1096.871 Million cell updates/sec

Title: US-09-905-589A-2
Perfect score: 2364
Sequence: 1 MRKISNHGSLRVAKVAYPLG.....ALGAIFHYIDSLNRQKSPAS 456

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	590.5	25.0	479	2	T23508	hypothetical prote
2	508	21.5	556	2	T39109	probable guanosine
3	498	21.1	518	2	A40732	guanosine-diphosph
4	485	20.5	454	2	JC4616	apyrase (EC 3.6.1.
5	442.5	18.7	455	2	S48859	nucleoside triphos
6	372	15.7	516	2	G84442	probable nucleosid
7	343	14.5	485	2	T34147	hypothetical prote
8	339.5	14.4	483	2	D86276	hypothetical prote
9	329.5	13.9	630	2	S50463	hypothetical prote
10	307	13.0	557	2	T16696	hypothetical prote
11	301	12.7	405	2	E86276	hypothetical prote
12	285.5	12.1	510	2	I56242	lymphoid cell acti
13	281.5	11.9	572	2	T40856	probable nucleotid
14	245.5	10.4	1052	2	T04439	hypothetical prote
15	219	9.3	508	2	C86276	7A19.33 protein -
16	140.5	5.9	628	2	A55421	nucleoside-triphos
17	111	4.7	679	2	C71007	probable formate d
18	108.5	4.6	1186	2	T12737	tail protein - Met
19	106.5	4.5	665	2	E75124	formate dehydrogen
20	104.5	4.4	322	2	T24948	hypothetical prote
21	103.5	4.4	322	2	T27308	hypothetical prote
22	102.5	4.3	440	2	I39847	cell-division prot
23	102	4.3	475	2	G72274	glutamyl tRNA-Gln
24	102	4.3	623	2	G81346	heat shock protein
25	102	4.3	4162	2	T42633	connectin/titin -
26	100	4.2	1233	2	T37045	nitrate reductase
27	100	4.2	26926	1	I38344	titin, cardiac mus
28	99.5	4.2	470	1	S13839	dihydrolipoamide d
29	99.5	4.2	504	2	S17724	H+-transporting tw
30	99.5	4.2	633	2	I39585	dnaK-type molecula
31	99.5	4.2	2411	2	A46299	tyrosine kinase su
32	98.5	4.2	633	2	AE2591	DNAK Protein [impo
33	98.5	4.2	633	2	E97373	dnaJ protein (heat
34	97.5	4.1	415	1	C64473	adenosylhomocystei
35	97.5	4.1	548	2	S32615	triacylglycerol li
36	97	4.1	2611	2	T14591	actinomycin synthe
37	96.5	4.1	815	2	T35970	probable efflux pr
38	96	4.1	711	2	S73898	DNA topoisomerase
39	96	4.1	1217	2	T25894	hypothetical prote
40	95.5	4.0	325	2	T32940	hypothetical prote
41	95.5	4.0	325	2	D87733	protein W03D8.9 [i
42	95	4.0	527	1	S25478	heat shock transcr
43	95	4.0	549	2	S23448	triacylglycerol li
44	95	4.0	15281	2	S41309	cyclosporin synthe
45	94.5	4.0	489	2	F97119	nicotinic acid pho

ALIGNMENTS

RESULT 1
T23508
hypothetical protein K08H10.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T23508
R;Gardner, A.
submitted to the EMBL Data Library, November 1996
A;Reference number: Z19750
A;Accession: T23508
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-479 <WIL>
A;Cross-references: UNIPROT:Q9XU84; EMBL:Z83113; PIDN:CAB05544.1; GSPDB:GN00023; CESP:K0
A;Experimental source: clone K08H10
C;Genetics:
A;Gene: CESP:K08H10.4
A;Map position: 5
A;Introns: 36/3; 83/3; 189/1; 300/2; 412/3
C;Superfamily: nucleoside triphosphatase chromatin-associated

Query Match 25.0%; Score 590.5; DB 2; Length 479;
Best Local Similarity 34.2%; Pred. No. 4.4e-40;
Matches 134; Conservative 78; Mismatches 155; Indels 25; Gaps 9;

```
Qy         73 FYGIMFDAGSTGTRVHVFQFTRPPRETP-----TLTHETFKAVKPGLSAYADDVEKSAQG 127
              |: |: ||||||||:|:::|    |          :  | |: ||||||::|     :|
Db         42 FFTIVIDAGSTGTRLHLYKFIHDPAIASHGMPFKVEKEIFQEVKPGLSSFAKSPSSAADS 101

Qy        128 IRELLDVAKQDIPFDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKE-VFKASPFLVGDD 186
              :  ||  |::::|    |: ||: ||||||||||||: |  :|: |:| :| :  |    |
Db        102 LEPLLQRARKEVPHFMWEKTPITLKATAGLRLLPGDMADDILESVEERIFNSGFFAAFPD 161

Qy        187 CVSIMNGTDEGVSAWITINFLTGSL---------KTPGGSSVGMLDLGGGSTQIAFLPRV 237
              |::| |:|||| :| |:| |  :|          |      ||   ||||||||: : |
Db        162 AVNVMPGSDEGVYSWFTLNILLETLFTDEPTVGHKPAAHRSVAAFDLGGGSTQLTYWPNN 221

Qy        238 EGTLQASPPGYLTALRMFNRTYKLYSYSYLGLGLMSARLAILGGVEGQPAKDGKELVSPC 297
              |  :   ||   :  |   :|:::|:|| ||::||| ||       :   :|:: |
Db        222 EAVF-SEHVGYERDIDFFGHHIRLFTHSFLGNGLIAARLNILQLETDNEIESTHQLITSC 280

Qy        298 LSPSFK-GEWEHAEVTYRVSGQKAAASLHELCAARVSEVLQ-NRVHRTEEVKHVDFYAFS 355
              :   ::  |||:|   : ::|  :::   | |       :: : :    |:|    | ||
Db        281 MPEGYQLTEWEYALKFWNING--SSSHSFESCYGTTKNFVESSEIMHLRELKGSPVYLFS 338

Qy        356 YYYDLAAGVGLIDAEKGGSLVVGDFEIAAKYVCRTLETQPQSS----PFSCMDLTYV-SL 410
              |::| |   ||:   :|| : :  |: ||:  ||  :|:         |: |:|||: ||
Db        339 YFFDRALNSGLVKGNEGGKIELRQFKEAAEIACRREKTEIDDGSHWMPWQCLDLTYIYSL 398

Qy        411 LLQEFGFPRSKVLKLTRKIDNVETSWALGAIF 442
              | : |  :: | | :||  :| ||  |  |
Db        399 LRDGYQFEDNQPLVLAKKIKGMEVSWGQGLAF 430
```

RESULT 2
T39109
probable guanosine-diphosphatase - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T39109
R;Barrell, B.G.; Rajandream, M.A.; Quail, M.; Seegar, K.; Harris, D.
submitted to the EMBL Data Library, October 1999
A;Reference number: Z21828
A;Accession: T39109
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-556 <BAR>
A;Cross-references: UNIPROT:Q9UT35; EMBL:AL121741; PIDN:CAB57338.1; GSPDB:GN00066; SPDB:
A;Experimental source: strain 972h-; cosmid c824
C;Genetics:
A;Gene: SPDB:SPAC824.08
A;Map position: 1

Query Match 21.5%; Score 508; DB 2; Length 556;
Best Local Similarity 32.4%; Pred. No. 2.8e-33;
Matches 142; Conservative 66; Mismatches 142; Indels 88; Gaps 17;

```
Qy         74 YGIMFDAGSTGTRVHVFQFTRPPRETPTLTHETFKAVKPGLSAYADDVEKSAQGIRELLD 133
              | :| ||||||:||||:||       :| |  | || ::||||::| | | :|  :  |||
Db        134 YVLMIDAGSTGSRVHVYQFNN-CNPSPKLEEEFFKMIEPGLSSFAGDPEGAAASLDPLLD 192

Qy        134 VAKQDIPFDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKAS-PFLVGDDCVSIMN 192
               | :::| :: : :|: :|||||||||    :|: :|: |::  :   || :  | |||:
Db        193 YAMENVPEEYRRCSPIAVKATAGLRLTGESEAKAILKSVRQHLENDYPFPIVKDGVSILE 252

Qy        193 GTDEGVSAWITINFLTGSLKTPGG----SSVGMLDLGGGSTQIAFLPRVEGTLQASPPG- 247
              |: ||: ||||||:| |:|   ||    |:| ::|||| |||: | ||     ::   |
Db        253 GSMEGIYAWITINYLLGTL---GGKATHSTVAVMDLGGASTQLVFEPRFASDGESLVDGD 309

Qy        248 YLTALRMFNRTYKLYSYSYLGLGLMSAR----------------LAILGGVEGQPAKDG 290
              :   |       |:|| :|:|| ||  ||                  | :||       |
Db        310 HKYVLDYNGEQYELYQHSHLGYGLKEARKLIHKFVLNNAEALKESLELLG--------DS 361

Qy        291 KELVSPCL-------SPSFKGEWEHAEVTYRVSGQKAAASLHELCAARVSEVLQ------ 337
              :: |||        |  |   | :|| : |    |  ||   |     : |
Db        362 TSIIHPCLHLNASLTHPDSKS--EASEVVF-VGPSLAHLSLQ--CRGIAEKALYKDKNCP 416

Qy        338 ------NRVHR---TEEVKHVDFYAFSYYYDLAAGVGLIDAEKGGSLVVGDFEIAAKYVC 388
                   | ||:   ||       |  ||:||    :|:       :  : | :  |  ||
Db        417 VRPCSFNGVHQPKFTETFTDSPIYLISYFYDRMISLGM-----PSTFTIEDMKYLANSVC 471

Qy        389 ----------------RTLETQPQSSPFSCMDLTY-VSLLLQEFGFPRSKVLKLTRKIDN 431
                             : |: :|:     |:|| | :|||   :  | :: |   :||||
Db        472 SGPTYWQDAFSLTDALKELKEEPE----WCLDLNYMISLLSVGYEIPNNRQLHTAKKIDN 527

Qy        432 VETSWALGAIFHYIDSLN 449
               |  | |||    :   |
Db        528 KELGWCLGASLSMLSEQN 545
```

RESULT 3
A40732
guanosine-diphosphatase (EC 3.6.1.42) - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein YEL042w
C;Species: Saccharomyces cerevisiae
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A40732; B40732; S30837; S50502
R;Abeijon, C.; Yanagisawa, K.; Mandon, E.C.; Hausler, A.; Moremen, K.; Hirschberg, C.B.;
J. Cell Biol. 122, 307-323, 1993
A;Title: Guanosine diphosphatase is required for protein and sphingolipid glycosylation
A;Reference number: A40732; MUID:93308137; PMID:8391537
A;Accession: A40732
A;Molecule type: DNA
A;Residues: 1-518 <ABE>
A;Cross-references: UNIPROT:P32621; EMBL:L19560; NID:g349392; PIDN:AAA34656.1; PID:g3493

A;Note: sequence extracted from NCBI backbone (NCBIN:134708, NCBIP:134711)
A;Accession: B40732
A;Molecule type: protein
A;Residues: 125-144;238-257;276-281;366-374;399-412 <AB2>
R;Mulligan, J.T.; Dietrich, F.S.; Hennessey, K.M.; Sehl, P.; Komp, C.; Wei, Y.; Taylor, F
submitted to the EMBL Data Library, February 1993
A;Reference number: S30812
A;Accession: S30837
A;Molecule type: DNA
A;Residues: 1-518 <MUL>
A;Cross-references: GB:U18779; EMBL:L10830; NID:g603625; PIDN:AAB65000.1; PID:g603637
R;Dietrich, F.S.
submitted to the EMBL Data Library, December 1994
A;Description: The sequence of S. cerevisiae cosmids 8199, 8334, and 9871.
A;Reference number: S50491
A;Accession: S50502
A;Molecule type: DNA
A;Residues: 1-518 <DIE>
A;Cross-references: EMBL:U18779; NID:g603625; PIDN:AAB65000.1; PID:g603637; MIPS:YEL042w
C;Genetics:
A;Gene: SGD:GDA1
A;Cross-references: SGD:S0000768; MIPS:YEL042w
A;Map position: 5L
C;Function:
A;Description: hydrolase
C;Superfamily: nucleoside triphosphatase chromatin-associated
C;Keywords: glycoprotein; Golgi apparatus; hydrolase; transmembrane protein
F;10-24/Domain: transmembrane #status predicted <TMM>
F;41,280,335/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 21.1%; Score 498; DB 2; Length 518;
Best Local Similarity 33.1%; Pred. No. 1.7e-32;
Matches 144; Conservative 60; Mismatches 153; Indels 78; Gaps 15;

```
Qy         65 TAADGHEVFYGIMFDAGSTGTRVHVFQF---TRPPRETPTLTHETFKAVKPGLSAYADDV 121
              | :: |:  | || ||||||:|||:::|   | |    |||  | |  ::|||::  |
Db         86 TCSEEHK--YVIMIDAGSTGSRVHIYKFDVCTSP----PTLLDEKFDMLEPGLSSFDTDS 139

Qy        122 EKSAQGIRELLDVAKQDIPFDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKE-VFKASP 180
               :|  :  || ||   :|      ||: :|||||||||    |: |:|  |:: : |  |
Db        140 VGAANSLDPLLKVAMNYVPIKARSCTPVAVKATAGLRLLGDAKSSKILSAVRDHLEKDYP 199

Qy        181 F-LVGDDCVSIMNGTDEGVSAWITINFLTGSLKTPGGS--SVGMLDLGGGSTQIAFLPRV 237
              | :|  | |||| | :||| |||| |:| |::   |    :  : |||||||| | |
Db        200 FPVVEGDGVSIMGGDEEGVFAWITTNYLLGNIGANGPKLPTAAVFDLGGGSTQIVFEPTF 259

Qy        238 EGTLQASPPGYLTALRMFNRTYKLYSYSYLGLGLMSARLAILGGVEGQPAKDGK------ 291
                :     :  |:  :  | || :|:|| ||   |  :   :     ||||
Db        260 PINEKMVDGEHKFDLKFGDENYTLYQFSHLGYGLKEGRNKVNSVLVENALKDGKILKGDN 319

Qy        292 ----ELVSPCLSPSFKGEWE----HAEVTYRV--------SGQKAAASLHELCAARVSEV 335
                  :| |||| |       |      :: || :         || :       |      |:
Db        320 TKTHQLSSPCLPPKVNATNEKVTLESKETYTIDFIGPDEPSGAQ--------CRFLTDEI 371

Qy        336 LQ-----------NRVHRTEEVKHV----DFYAFSYYYDLAAGVGLIDAEKGGSLVVGD 379
              |           | ||:   |:       | | |||:||    :|:       |  : :
Db        372 LNKDAQCQSPPCSFNGVHQPSLVRTFKESNDIYIFSYFYDRTRPLGM-----PLSFTLNE 426

Qy        380 FEIAAKYVCRTLET------------QPQSSPFSCMDLTY-VSLLLQEFGFPRSKVLKL 425
               |: ||:  ||               : :|    |:||:: ||||   :  |  : |:
Db        427 LNDLARIVCKGEETWNSVFSGIAGSLDELESDSHFCLDLSFQVSLLHTGYDIPLQRELRT 486

Qy        426 TRKIDNVETSWALGA 440
               :|| | |  | |||
Db        487 GKKIANKEIGWCLGA 501
```

RESULT 4
JC4616
apyrase (EC 3.6.1.5) precursor - potato
N;Alternate names: adenylpyrophosphatase; ATP-diphosphohydrolase
C;Species: Solanum tuberosum (potato)
C;Date: 10-May-1996 #sequence_revision 19-Jul-1996 #text_change 09-Jul-2004

C;Accession: JC4616; PC4147
R;Handa, M.; Guidotti, G.
Biochem. Biophys. Res. Commun. 218, 916-923, 1996
A;Title: Purification and cloning of a soluble ATP-diphosphohydrolase (Apyrase) from pot
A;Reference number: JC4616; MUID:96158985; PMID:8579614
A;Accession: JC4616
A;Molecule type: mRNA
A;Residues: 1-454 <HAN>
A;Cross-references: UNIPROT:P80595; GB:U58597; NID:g1381632; PIDN:AAB02720.1; PID:g13816
A;Accession: PC4147
A;Molecule type: protein
A;Residues: 59-95;96-131;132-160;236-253;332-345 <HA2>
A;Experimental source: tubers
A;Note: The authors translated the codon GCA for residue 215 as Gly
C;Comment: This enzyme belongs to a family of E-type ATPases, and it catalyzes the hydro
 enzyme has nucleotide substrate specificity, divalent cation requirement, and insensiti
olved in starch synthesis.
C;Genetics:
A;Gene: rrop1
C;Superfamily: nucleoside triphosphatase chromatin-associated
C;Keywords: glycoprotein; hydrolase; transmembrane protein
F;1-30/Domain: signal sequence #status predicted <SIG>
F;8-25/Domain: transmembrane #status predicted <TMM>
F;31-454/Product: ATP-diphosphohydrolase #status predicted <MAT>
F;44-65/Region: actin-heat shock protein 70-hexokinase beta-phosphate binding
F;44-65/Region: nucleotide binding #status predicted
F;192-212/Region: actin-heat shock protein 70-hexokinase gamma-phosphate binding
F;192-212/Region: nucleotide binding #status predicted
F;390-410,427-446/Region: hydrophobic carboxyl end
F;151,262/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match 20.5%; Score 485; DB 2; Length 454;
  Best Local Similarity 31.9%; Pred. No. 1.6e-31;
  Matches 138; Conservative 68; Mismatches 183; Indels 44; Gaps 12;

```
Qy         59 AHSPLGTAADGHE-VFYGIMFDAGSTGTRVHVFQFTRPPRETPTLTH-ETFKAVKPGLSA 116
Db         30 AQIPLRRHLLSHESEHYAVIFDAGSTGSRVHVFRFDEKLGLLPIGNNIEYFMATEPGLSS 89

Qy        117 YADDVEKSAQGIRELLDVAKQDIPFDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVF 176
Db         90 YAEDPKAAANSLEPLLDGAEGVVPQELQSETPLELGATAGLRMLKGDAAEKILQAVRNLV 149

Qy        177 K-ASPFLVGDDCVSIMNGTDEGVSAWITINFLTGSLKTPGGSSVGMLDLGGGSTQIAFLP 235
Db        150 KNQSTFHSKDQWVTILDGTQEGSYMWAAINYLLGNLGKDYKSTTATIDLGGGSVQMAYAI 209

Qy        236 RVEGTLQA----SPPGYLTALRMFNRTYKLYSYSYLGLGLMSARLAILGGVEGQPAKDGK 291
Db        210 SNEQFAKAPQNEDGEPYVQQKHLMSKDYNLYVHSYLNYGQLAGRAEIF--------KASR 261

Qy        292 ELVSPCLSPSFKGEWEHAEVTYRVSGQKAAASLHELCAARVSEVLQ-NRVHRTEEVK--- 347
Db        262 NESNPCALEGCDGYYSYGGVDYKVKAPKKGSS-WKRCRRLTRHALKINAKCNIEECTFNG 320

Qy        348 ---------HVDFYAFSYYYDLAAGVGLIDAEKGGSLVVG-DFEIAAKYVCRT------- 390
Db        321 VWNGGGGDGQKNIHASSFFYDIGAQVGIVDTKFPSALAKPIQYLNAAKVACQTNVADIKS 380

Qy        391 --LETQPQSSPFSCMDLTY-VSLLLQEFGFPRSKVLKLTRKIDN----VETSWALGAIFH 443
Db        381 IFPKTQDRNIPYLCMDLIYEYTLLVDGFGLNPHKEITVIHDVQYKNYLVGAAWPLGCAID 440

Qy        444 YIDSLNRQKSPAS 456
Db        441 LVSSTTNKIRVAS 453
```

RESULT 5
S48859
nucleoside triphosphatase precursor, chromatin-associated - garden pea
C;Species: Pisum sativum (garden pea)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: S65147; S48859
R;Hsieh, H.L.; Tong, C.G.; Thomas, C.; Roux, S.J.
Plant Mol. Biol. 30, 135-147, 1996
A;Title: Light-modulated abundance of an mRNA encoding a calmodulin-regulated, chromatin-
A;Reference number: S65141; MUID:96197404; PMID:8616230
A;Accession: S65147
A;Molecule type: mRNA
A;Residues: 1-455 <HS2>
A;Cross-references: UNIPROT:P52914; EMBL:Z32743; NID:g563611; PIDN:CAA83655.1; PID:g5636
C;Superfamily: nucleoside triphosphatase chromatin-associated
C;Keywords: nucleus

  Query Match 18.7%; Score 442.5; DB 2; Length 455;
  Best Local Similarity 29.2%; Pred. No. 4.6e-28;
  Matches 125; Conservative 79; Mismatches 145; Indels 79; Gaps 15;

```
Qy         74 YGIMFDAGSTGTRVHVFQFTRPPRETPTLTH-----ETFKAVKPGLSAYADDVEKSAQGI 128
Db         44 YAVVFDAGSTGSRIHVYHF----NQNLDLLHIGKGVEYYNKITPGLSSYANNPEQAAKSL 99

Qy        129 RELLDVAKQDIPFDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVF-KASPFLVGDDC 187
Db        100 IPLLEQAEDVVPDDLQPKTPVRLGATAGLRLLNGDASEKILQSVRDMLSNRSTFNVQPDA 159

Qy        188 VSIMNGTDEGVSAWITINFLTGSLKTPGGSSVGMLDLGGGSTQIAF---------LPRVE 238
Db        160 VSIIDGTQEGSYLWVTVNYALGNLGKKYTKTVGVIDLGGGSVQMAYAVSKKTAKNAPKV- 218

Qy        239 GTLQASPPGYLTALRMFNRTYKLYSYSYLGLGLMSARLAILGGVEGQPAKDGKELVSPCL 298
Db        219 --ADGDDP-YIKKVVLKGIPYDLYVHSYLHFGREASRAEILKLTPRSP--------NPCL 267

Qy        299 SPSFKGEWEHAEVTYRVSGQKAAASLHELCAARVSEVLQNRVHRTEEVKH---------- 348
Db        268 LAGFNGIYTYSGEEFKATAYTSGANFNK---------CKNTIRKALKLNYPCPYQNCTFG 318

Qy        349 -----VDFYAFSYYYDLAAGVGLIDAEKGGSLV-VGDFEIAAKYVCR-TLETQP 395
Db        319 GIWNGGGGNGQKNLFASSSFFYLPEDTGMVDASTPNFILRPVDIETKAKEACALNFEDAK 378

Qy        396 QSSPF---------SCMDLTYVSLLLQEFGFPRSKVLKLT--RKIDN----VETSWALGA 440
Db        379 STYPFLDKKNVASYVCMDLIYQYVLLVD-GFGLDPLQKITSGKEIEYQDAIVEAAWPLGN 437

Qy        441 IFHYIDSL 448
Db        438 AVEAISAL 445
```

RESULT 6
G84442
probable nucleoside triphosphatase [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C;Accession: G84442
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: G84442
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-516 <STO>
A;Cross-references: UNIPROT:O80612; GB:AE002093; NID:g3461821; PIDN:AAC32915.1; GSPDB:GN
C;Genetics:
A;Gene: At2g02970
A;Map position: 2
C;Superfamily: nucleoside triphosphatase chromatin-associated

  Query Match 15.7%; Score 372; DB 2; Length 516;
  Best Local Similarity 29.0%; Pred. No. 3e-22;

```
  Matches  113;  Conservative   67;  Mismatches  173;  Indels   36;  Gaps   13;

Qy         74 YGIMFDAGSTGTRVHVFQFT----RPPRETPTLTHETFKAVKPGLSAYADDVEKSAQGIR 129
Db         68 YSVVIDGGSTGTRIHVFGYRIESGKPVFEFRGANYASLK-LHPGLSAFADDPDGASVSLT 126

Qy        130 ELLDVAKQDIPFDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASPFLVGDDCVS 189
Db        127 ELVEFAKGRVPKGMWIETEVRLMATAGMRLLELPVQEKILGVARRVLKSSGFLFRDEWAS 186

Qy        190 IMNGTDEGVSAWITINFLTGSLKTPGGSSVGMLDLGGGSTQIAFLPRVEGTLQASPPGYL 249
Db        187 VISGSDEGVYAWVVANFALGSLGGDPLKTTGIVELGGASAQVTFV-----SSEPMPPEFS 241

Qy        250 TALRMFNRTYKLYSYSYLGLGLMSARLAILGGVEG-------QPAKDGKELVSPCLSPSF 302
Db        242 RTISFGNVTYNLYSHSFLHFGQNAAHDKLWGSLLSRDHNSAVEPTRE-KIFTDPCAPKGY 300

Qy        303 K---GEWEH-----AEVTYRVSGQKAAASLHELCAARVSEVLQNRVHRTEEVKHVDFYAF 354
Db        301 NLDANTQKHLSGLLAEES-RLSDSFQAGGNYSQCRSAALTILQDGNGRI----LIIIAGF 355

Qy        355 SY-YYDLAAGVGLIDAEKGGSLVVGDFEIAAKYVCRTLETQPQSSPFSCMDLTY-VSLLL 412
Db        356 SFLFFGLGEKAWLSNMISAGERFCG--EDWSKLRVKDPSLHEEDLLRYCFSSAYIVSLLH 413

Qy        413 QEFGFP-RSKVLKLTRKIDNVETSWALGA 440
Db        414 DTLGIPLDDERIGYANQAGDIPLDWALGA 442
```

RESULT 7
T34147
hypothetical protein C33H5.14 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C;Accession: T34147
R;Bradshaw, H.; Stellyes, L.
submitted to the EMBL Data Library, November 1995
A;Description: The sequence of C. elegans cosmid C33H5.
A;Reference number: Z21482
A;Accession: T34147
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-485 <BRA>
A;Cross-references: UNIPROT:Q18411; EMBL:U41007; PIDN:AAA82272.1; CESP:C33H5.14
A;Experimental source: strain Bristol N2
C;Genetics:
A;Gene: CESP:C33H5.14
A;Introns: 22/1; 83/1; 120/2; 167/1; 269/3; 399/3
C;Superfamily: nucleoside triphosphatase chromatin-associated

```
  Query Match             14.5%;  Score 343;  DB 2;  Length 485;
  Best Local Similarity   25.8%;  Pred. No. 6.3e-20;
  Matches  113;  Conservative   74;  Mismatches  157;  Indels   94;  Gaps   16;

Qy         70 HEVFYGIMFDAGSTGTRVHVFQFTRPP-----RETPTLTHET---FKAVKPGLSAYADDV 121
Db         21 NNIKYGVICDAGSSGTR--LFVYTLKPLSGGLTNIDTLIHESEPVVKKVTPGLSSFGDKP 78

Qy        122 EKSAQGIRELLDVAKQDIPFDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASPF 181
Db         79 EQVVEYLTPLLRFAEEHIPYEQLGETDLLIFATAGMRLLPEAQKDAIIKNLQNGLKSVTA 138

Qy        182 L-VGDDCVSIMNGTDEGVSAWITINFLTGSLKTPGGSSVGMLDLGGGSTQIAFLPRVEGT 240
Db        139 LRVSDSNIRIIDGAWEGIYSWIAVNYILGRFDKENDSKVGMIDMGGASVQIAF--EIANE 196

Qy        241 LQASPPGYLTALRM------FNRTYKLYSYSYLGLGLMSARLAILGGVEGQPAKDGKELV 294
Db        197 KESYNGGNVYEINLGSIETNEDYKYKIYSTTFLGYGANEG----LKKYENSLVKSGNS-- 250

Qy        295 SPCLSP------------SFKGEWEHAEVTYRVSGQKAAASLHELCAARVSEV------- 335
Db        251 NDSCSPRGLNRLIGEFTVNGTGEW-------------------DVCLAQVSSLIGDKAQP 291

Qy        336 --------LQNRVHRTEEVKHVDFYAFSYYYDLAAGVGLIDAEKGGSLVVGDFEIAAKYV 387
Db        292 SCPNPTCFLRNVIAPSVNLSTVQLYGFSEYWYTTSNFG-----SGGEYHYQKFTDEVRKY 346

Qy        388 CR----TLETQPQSSPF----------SCMDLTYVSLLLQEFGFPRSKVLKLTR---KID 430
Db        347 CQKDWNDIQDGFKRNEFPNADIERLGTNCFKAAWVTSVLHD-GFNVDKTKHLFQSVLKIA 405

Qy        431 NVETSWALGAIFHYIDSL 448
Db        406 GEEMQWALGAMLYHSKDL 423
```

RESULT 8
D86276
hypothetical protein F7A19.34 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: D86276
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, L
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: D86276
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-483 <STO>
A;Cross-references: UNIPROT:Q9XI62; GB:AE005172; NID:g5080801; PIDN:AAD39311.1; GSPDB:GN
C;Genetics:
A;Map position: 1
C;Superfamily: nucleoside triphosphatase chromatin-associated

```
  Query Match             14.4%;  Score 339.5;  DB 2;  Length 483;
  Best Local Similarity   26.5%;  Pred. No. 1.2e-19;
  Matches  108;  Conservative   78;  Mismatches  166;  Indels   55;  Gaps   13;

Qy         74 YGIMFDAGSTGTRVHVFQF----TRPPRETPTLTHETFKAVKPGLSAYADDVEKSAQGIR 129
Db         70 YSVLIDAGSSGTRVHVFGYWFESGKPVFDFGEKHYANLK-LTPGLSSYADNPEGASVSVT 128

Qy        130 ELLDVAKQDIPFDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASPFLVGDDCVS 189
Db        129 KLVEFAKQRIPKRMFRRSDIRLMATAGMRLLEVPVQEQILEVTRRVLRSSGFMFRDEWAN 188

Qy        190 IMNGTDEGVSAWITINFLTGSLKTPGGSSVGMLDLGGGSTQIAFLPRVEGTLQASPPGYL 249
Db        189 VISGSDEGIYSWITANYALGSLGTDPLETTGIVELGGASAQVTFV-----SSEHVPPEYS 243

Qy        250 TALRMFNRTYKLYSYSYLGLG-----------LMSARLAILGGVEGQPA--------KDG 290
Db        244 RTIAYGNISYTIYSHSFLDYGKDAALKKLLEKLQNSANSTVDGVVEDPCTPKGYIYDTNS 303

Qy        291 KELVSPCLS--PSFKGEWEHA-------EVTYRVSGQKAAASLHELCA--ARVSEVLQNR 339
Db        304 KNYSSGFLADESKLKGSLQAAGNFSKCRSATFALLKEGKENCLYEHCSIGSTFTPDLQGS 363

Qy        340 VHRTEEVKHVDFYAFSYYYDLAAGVGLIDAEKGGSLVVGDFEIAAKYVCRTLETQPQSSP 399
Db        364 FLAT-----ASFYYTAKFFELEEKGWLSELIPAGKRYCG--EEWSKLILEYPTTDEEYLR 416

Qy        400 FSCMDLTY-VSLLLQEFGFPR-----SKVLKLTRKIDNVETSWALGA 440
Db        417 GYCFSAAYTISMLHDSLGIALDDESITYASKAGEK--HIPLDWALGA 461
```

```
RESULT 9
S50463
hypothetical protein YER005w - yeast (Saccharomyces cerevisiae)
C;Species: Saccharomyces cerevisiae
C;Date: 28-May-1993 #sequence_revision 24-Feb-1995 #text_change 09-Jul-2004
C;Accession: S50463
R;Dietrich, F.S.
submitted to the EMBL Data Library, December 1994
A;Description: The sequence of S. cerevisiae cosmids 9537, 9581, 9495, 9867, and lambda
A;Reference number: S50433
A;Accession: S50463
A;Molecule type: DNA
A;Residues: 1-630 <DIE>
A;Cross-references: UNIPROT:P40009; EMBL:U18778; NID:g603592; PID:g603597; GSPDB:GN00005
C;Genetics:
A;Gene: SGD:YND1; MIPS:YER005w
A;Cross-references: SGD:S0000807
A;Map position: 5R

  Query Match            13.9%;  Score 329.5;  DB 2;  Length 630;
  Best Local Similarity  26.9%;  Pred. No. 1.1e-18;
  Matches  122;  Conservative   72;  Mismatches  163;  Indels   97;  Gaps   22;

Qy         74 YGIMFDAGSTGTRVHVFQFTRPPRETPTLTHE--------------------TFKAVKP 112
              :||: ||||:|:|:|||::    ::| :| |                      ||| : |
Db         10 FGIVIDAGSSGSRIHVFKW----QDTESLLHATNQDSQSILQSVPHIHQEKDWTFK-LNP  64

Qy        113 GLSAYADDVEKSAQG-----IRELLDVAKQDIPFDFWKATPLVLKATAGLRLLPGEKAQK 167
              |||::    ||  |       }: ||| ||  ||   | : |: ::||||:|||| :
Db         65 GLSSF----EKKPQDAYKSHIKPLLDFAKNIIPESHWSSCPVFIQATAGMRLLPQDIQSS 120

Qy        168 LLQKVKEVFK-ASPFLVGDDC---VSIMNGTDEGVSAWITINFLTGSLK--TPGGS---S 218
              :|  : :  |  : ||| :||    : :::|  ||:  |: :|:| |       |  |   :
Db        121 ILDGLCQGLKHPAEFLV-EDCSAQIQVIDGETEGLYGWLGLNYLYGHFNDYNPEVSDHFT 179

Qy        219 VGMLDLGGGSTQIAFLPRVEGTLQASPPGYLTA-LRMFN---RTYKLYSYSYLGLGLMSA 274
              | :|:|| ||||||  |   | :          |  ||  |   : : ::  ::|| |   |
Db        180 FGFMDMGGASTQIAFAPHDSGEIARHRDDIATIFLRSVNGDLQKWDVFVSTWLGFGANQA 239

Qy        275 R---LAILGGVEGQPAKD-------GKELVSPCLSPSFKGEWEHAEVTYRVSG----QKA 320
              |   || |    :   |          : |  }|:       ::|  :  : ::|    ::
Db        240 RRRYLAQLINTLPENTNDYENDDFSTRNLNDPCMPRGSSTDFEFKDTIFHIAGSGNYEQC 299

Qy        321 AASLHELCAARV----SEVLQNRVHRTE-EVKHVDFYAFSYYYDLAAGVGLIDAEKGGSL 375
              |:: |    :       | | ||    :  :  |    | |:  |  |      : ||
Db        300 TKSIYPLLLKNMPCDDEPCLFNGVHAPRIDFANDKFIGTSEYWYTANDV----FKLGGEY 355

Qy        376 VVGDFEIAAKYVCRTLETQ-------------PQS-SPFSCMDLTYVSLLLQE-FGFPRS 420
                |  : :  | :  ||              |::    :|    :|  :| | |  ||
Db        356 NFDKFSKSLREFCNSNWTQILANSDKGVYNSIPENFLKDACFKGNWVLNILHEGFDMPRI 415

Qy        421 KV----------LKLTRKIDNVETSWALGAIFHY 444
              |           :   |::  | || || |  |
Db        416 DVDAENVNDRPLFQSVEKVEERELSWTLGRILLY 449


RESULT 10
T16696
hypothetical protein R07E4.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C;Accession: T16696
R;Miller, N.
submitted to the EMBL Data Library, October 1995
A;Description: The sequence of C. elegans cosmid R07E4.
A;Reference number: Z18561
A;Accession: T16696
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-557 <MIL>
A;Cross-references: EMBL:U39652; NID:g1049390; PID:g1049394; PIDN:AAA80403.1; CESP:R07E4
A;Experimental source: strain Bristol N2
C;Genetics:
A;Gene: CESP:R07E4.4
A;Introns: 39/1; 67/1; 145/2; 192/1; 244/3; 317/3; 451/3; 488/2

  Query Match            13.0%;  Score 307;  DB 2;  Length 557;
  Best Local Similarity  23.5%;  Pred. No. 6.5e-17;
  Matches  119;  Conservative   88;  Mismatches  178;  Indels  122;  Gaps   23;

Qy         13 AKVAYPLGLCVGVFIYVAYIKWHRATATQAFFSITRAAPGARWGQQAHSPLGTAADGHEV 72
              | : :|    | |||||                                :||:    ||  |
Db         14 AMIFFP----VIVFIYVV--------------------------EAHTSPKVIADDQER 42

Qy         73 FYGIMFDAGSTGTRVHVFQFTRPP-----RETPTL--THETFKAVKPGLSAYADDVEKSA 125
              ||:: ||||||||: |: :          :  | :        | : |||| :     ::|
Db         43 SYGVICDAGSTGTRLFVYNWISTSDSELIQIEPVIYDNKPVMKKISPGLSTFGTKPAQAA 102

Qy        126 QGIRELLDVAKQDIPFDFWKATPLVLKATAGLRLLP------GEKAQKLLQKVKEVFKAS 179
              : :| |:::|:: || :    ||: : ||||:||:|       |:|   |      :: | :
Db        103 EYLRPLMELAERHIPEEKRPYTPVFIFATAGMRLIPDEYVLIGQKEAVLKNLRNKLPKIT 162

Qy        180 PFLVGDDCVSIMNGTDEGVSAWITINFL------TGSLKTPGGS-------SVGMLDLGG 226
                |  : :  |: |  ||: :|| :|:       | :|  || |       :|||:|:||
Db        163 SMQVLKEHIRIIEGKWEGIYSWIAVNYALGKFNKTATLDFPGTSPAHARQKTVGMIDMGG 222

Qy        227 GSTQIAF-LPRVEGTLQASPPGYLTALR----MFNRTYKLYSYSYLGL----GLMSARLA 277
              | |||| ||  :      :          |    :|  |||:  ::||     |:
Db        223 ASAQIAFELPDTDSFSSINVENINLGCREDDSLFK--YKLFVTTFLGYGVNEGIRKYEHM 280

Qy        278 ILGGVEGQPAKDGKELVSPCLSPSFKGEWEHAEVTYRVSGQ---KAAASLHELCAARVSE 334
              :|  :: |   :|  :   |:  :       |  ||   :|:   :          |:  | :
Db        281 LLSKLKDQ---NGTVIQDDCMPLNL-----HKTVTLE-NGENFVRRGTGNWNTCSNEVKK 331

Qy        335 VL----QNRVHRTEEVK--------------HVDFYAFS-YYYDLAAGVGLIDAEKGGSL 375
              :|     : | : |  |               ::: | || |:|     :||      ||
Db        332 LLNPESSSEVCKAEAAKCYFGAVPAPSIPLSNIEMYGFSEYWYSTHDVLGL-----GGQY 386

Qy        376 VVGDFEIAAKYVC----RTLETQPQSSPF----------SCMDLTYVSLLLQEFGFPRSK 421
              :      :  |      |:: : :   :           |    ::: :| : ||   |
Db        387 DAENIAKKTQQYCSKRWSTIQAESKKQLYPRADEERLRTQCFKSAWITSVLHD-GFSVDK 445

Qy        422 VLKLTRKIDNV---ETSWALGAIFHYI 445
                  : :  :   |  |||||: :::
Db        446 THNKFQSVSTIAGQEVQWALGAMIYHM 472


RESULT 11
E86276
hypothetical protein F14L17.1 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: E86276
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: E86276
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-405 <STO>
A;Cross-references: UNIPROT:Q9M9T7; GB:AE005172; NID:g7262666; PIDN:AAF43924.1; GSPDB:GN(
C;Genetics:
A;Map position: 1

  Query Match            12.7%;  Score 301;  DB 2;  Length 405;
  Best Local Similarity  25.4%;  Pred. No. 1.3e-16;
```

```
  Matches  104;  Conservative   65;  Mismatches  181;  Indels   60;  Gaps   13;

Qy         74 YGIMFDAGSTGTRVHVFQFTRPPRETPTLTHETFKAVKPGLSAYADDVEKSAQGIRELLD 133
Db          4 FGYWFESGKP-----VFDFGE--------EHYASLKLSPGLSSYADNPEGASVSVTKLVE 50

Qy        134 VAKQDIPFDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASPFLVGDDCVSIMNG 193
Db         51 FAKGRIPKGKLKKSDIRLMATAGMRLLDVPVQEQILDVTRRVLRSSGFKFQDEWATVISG 110

Qy        194 TDEGVSAWITINFLTGSLKTPGGSSVGMLDLGGGSTQIAFLPRVEGTLQASPPGYLTALR 253
Db        111 TDEGIYAWVVANHALGSLGGDPLKTTGIVELGGASAQVTFVPS-----EHVPPEFSRTIS 165

Qy        254 MFNRTYKLYSYSYLGLGLMSARLAILGGVEGQ-PAKDGKELV-SPCL------------- 298
Db        166 YGNVSYTIYSHSFLDFGQDAAEDKLLESLQNSVAASTGDGIVEDPCTPKGYIYDTHSQKD 225

Qy        299 SPSFKGEWEHAEVTYRVSGQKAAASLHELCAARVSEVLQNRVHRTEEVKHV--------- 349
Db        226 SSGFLSE----ESKFKASLQVQAAGDFTKCRSATLAMLQEGKENC-AYKHCSIGSTFTPN 280

Qy        350 ---DFYAFSYYYDLAAGVGLIDAEKGGSLVVGDFEIAAKYVCRTLETQPQSSP----FSC 402
Db        281 IQGSFLATENFFHTSKFFGLGEKEWLSEMILAGKRFCGEEWSKLKEKYPTTKDKYLHRYC 340

Qy        403 MDLTY-VSLLLQEFGF----PRSKVLKLTRKIDNVETSWALGAIFHYIDS 447
Db        341 FSSAYIISMLHDSLGVALDDERIKYASKAGK-ENIPLDWALGAFILNTDT 389
```

RESULT 12
I56242
lymphoid cell activation antigen - human
C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: I56242
R;Maliszewski, C.R.; Delespesse, G.J.; Schoenborn, M.A.; Armitage, R.J.; Fanslow, W.C.;
J. Immunol. 153, 3574-3583, 1994
A;Title: The CD39 lymphoid cell activation antigen. Molecular cloning and structural cha
A;Reference number: I56242; MUID:95015846; PMID:7930580
A;Accession: I56242
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-510 <RES>
A;Cross-references: UNIPROT:P49961; GB:S73813; NID:g765255; PIDN:AAB32152.1; PID:g765256
C;Superfamily: nucleoside triphosphatase chromatin-associated

```
  Query Match             12.1%;  Score 285.5;  DB 2;  Length 510;
  Best Local Similarity   26.2%;  Pred. No. 3.2e-15;
  Matches  114;  Conservative   68;  Mismatches  158;  Indels   95;  Gaps   20;

Qy         72 VFYGIMFDAGSTGTRVHVFQFTRPPRETPTLTH--ETFKAVKPGLSAYADDVEKSAQGIR 129
Db         47 VKYGIVLDAGSSHTSLYIYKWPAEKENDTGVVHQVEECRVKGPGISKFVQKVNEIGIYLT 106

Qy        130 ELLDVAKQDIPFDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKAS----PFLVGD 185
Db        107 DCMERAREVIPRSQHQETPVYLGATAGMRLLRME-SEELADRVLDVVERSLSNYPF--DF 163

Qy        186 DCVSIMNGTDEGVSAWITINFLTGSL-------------KTPGGSSVGMLDLGGGSTQIAF 233
Db        164 QGARIITGQEEGAYGWITINYLLGKFSQKTRWFSIVPYETNNQETFGALDLGGASTQVTF 223

Qy        234 LPRVEGTLQASPPGYLTALRMFNRTYKLYSYSYLGLGLMSARLAILGGVEGQPAKD---- 289
Db        224 VPQNQ-TIES--PDNALQFRLYGKDYNVYTHSFLCYGKDQALWQKL--------AKDIQVA 273

Qy        290 -GKELVSPCLSPSFKGE-----------WEHAEVT-----YRVSG----QKAAASLHEL- 327
Db        274 SNEILRDPCFHPGYKKVVNVSDLYKTPCTKRFEMTLPFQQFEIQGIGNYQQCHQSILELF 333

Qy        328 ---------CAAR--VSEVLQNRVHRTEEVKHVDFYAFSYYYDLAAGVGLIDAEKGGSLV 376
```

```
Db        334 NTSYCPYSQCAFNGIFLPPLQG----------DFGAFSAFYFVMKFLNLTSEKVSQEKV 382

Qy        377 VGDFEIAAKYVCRTLETQPQS---------SPFSCMDLTYV-SLLLQEFGFPRS--KVLK 424
Db        383 T---EMMKKFCAQPWEEIKTSYAGVKEKYLSEY-CFSGTYILSLLLQGYHFTADSWEHIH 438

Qy        425 LTRKIDNVETSWALG 439
Db        439 FIGKIQGSDAGWTLG 453
```

RESULT 13
T40856
probable nucleotide phosphatase - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T40856
R;Ramsperger, U.; Pohl, T.; Wood, V.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, October 1999
A;Reference number: Z21952
A;Accession: T40856
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-572 <RAM>
A;Cross-references: UNIPROT:Q9USP2; EMBL:AL121783; PIDN:CAB57847.1; GSPDB:GN00068; SPDB:S
A;Experimental source: strain 972h-; cosmid c11E10
C;Genetics:
A;Gene: SPDB:SPCC11E10.05c
A;Map position: 3

```
  Query Match             11.9%;  Score 281.5;  DB 2;  Length 572;
  Best Local Similarity   24.1%;  Pred. No. 8e-15;
  Matches  111;  Conservative   64;  Mismatches  164;  Indels  121;  Gaps   15;

Qy         74 YGIMFDAGSTGTRVHVFQFTRPPRETPTLTHETFK-----------------AVKPGLSA 116
Db          5 YGIFIDAGSSGSRLLIYSW---DYDTDSSLSDKVKKLPLIETGIGDGGKWSLKVQPGISS 61

Qy        117 YADDVEK-SAQGIRELLDVAKQDIPFDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEV 175
Db         62 FANNPKHVGKKHLKELLDFAAHAIPKDVHKETPVFLSATAGMRLLGVDAQNKILSHACRY 121

Qy        176 FKASPFLVGDDC---VSIMNGTDEGVSAWITINFLTGSLKTPGGSSVGMLDLGGGSTQIA 232
Db        122 IKKNYDFDIPNCSNSIRVIDGKAEGMYGWLATNYLLKTLEEKDTSTVGFLDMGGASVQIA 181

Qy        233 FLPRVEGTLQASPPGYLTALRMFNRT------------YKLYSYSYLGLGLMSARLAILG 280
Db        182 F---------ELPPSQLKNYKDSISTVHIGLQNGQQLEYPLFVTTWLGFGANEAYRRYLG 232

Qy        281 -GVEGQPAKDGKELVSPCLSPSFKGEWEHAEVTYRVSGQKAAASLHELCAARVSEVLQNR 339
Db        233 LLIESENGKVGNTLSDPC---SLRGR------TYDIDGIEFAGTGDLKQCLKLTYNLLNK 283

Qy        340 --------------------VHRTEEVKHVDF-YAFSYYYDLAAGVGLIDAEKGGSLVVG 378
Db        284 DKPCSMDPCNFDGISIPPVDFANTEFVGVSEFWYTTNDVFDM-----------GGSYHFP 332

Qy        379 DFEIAAKYVCRT-----------LETQPQSSPFSCMDLTY-----VSLLLQEFGFPRSKV 422
Db        333 NFYKKVDEYCGTEWETMLSRLYNKELTPSTDENKLEKLCFKASWALNVLHEGFDVPKSNT 392

Qy        423 ------------------LKLTRKIDNVETSWALGAIFHY 444
Db        393 SSNDAKDGLSVIPAYHSPFTSLEKIERTEVSWTLGQVLLY 432
```

RESULT 14
T04439
hypothetical protein T18B16.150 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 09-Jul-2004

```
C;Accession: T04439
R;Bevan, M.; Benes, V.; Rechmann, S.; Borkova, D.; Ansorge, W.; Bancroft, I.; Mewes, H.W
submitted to the Protein Sequence Database, April 1998
A;Reference number: Z15359
A;Accession: T04439
A;Molecule type: DNA
A;Residues: 1-1052 <BEV>
A;Cross-references: UNIPROT:O49676; EMBL:AL021687
A;Experimental source: cultivar Columbia; BAC clone T18B16
C;Genetics:
A;Map position: 4
A;Introns: 79/3; 118/3; 217/1; 295/3; 396/3; 531/2; 815/3
A;Note: T18B16.150

  Query Match             10.4%;  Score 245.5;  DB 2;  Length 1052;
  Best Local Similarity   25.3%;  Pred. No. 1.6e-11;
  Matches  116;  Conservative   60;  Mismatches  185;  Indels   97;  Gaps   20;

Qy         55 WGQQAHS--------PLGTAADGHE------------VFYGIMFDAGSTGTRVHVFQFT 93
              |||  |        | ||                  :|  :::    |||| :|:| :
Db        483 WGQNGSSFSKEKGSVPNGTNPSTRRKLIRAVMIVMCLFLFAFLVYIVSITGTRAYVYQAS 542

Qy         94 ---RPPRETPTLTHETFKAV-------------KPGLSAYADDVEKSAQGIRELLDVAK 136
                 :    | :     : :               :||     ::       |: |:  |:
Db        543 INYKKDSSLPIVMKSLTEGISRKSRGRAYDRMETEPGFDKLVNNRTGLKTAIKPLIQWAE 602

Qy        137 QDIPFDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASPFLVGDDCVSIMNGTDE 196
              : || :  : | | : ||||:| |    :  :| |  :    |||    : | |::||:|
Db        603 KQIPKNAHRTTSLFVYATAGVRRLRPADSSWILGNVWSILAKSPFTCRREWVKIISGTEE 662

Qy        197 GVSAWITINFLTGSL-KTPGGSSVGMLDLGGGSTQIAFLPRVEGTLQASPPGYLTALRMF 255
                |  :|: |  |   |  |  :: | ||||| | |: |    |   :     |  ||:
Db        663 AYFGWTALNYQTSMLGALPKKATFGALDLGGSSLQVTF----ENEERTHNETNLN-LRIG 717

Qy        256 NRTYKLYSYSYLGLGLMSA-------RLAILGGVEGQPAKDGK-ELVSPCLSPSFKGEWE 307
              :  : | :||  | ||  |       |  |  |      :|| |:  |||:  : |::
Db        718 SVNHHLSAYSLAGYGLNDAFDRSVVHLLKKLPNVNKSDLIEGKLEMKHPCLNSGYNGQYI 777

Qy        308 HAEVTYRVSGQKAAASLHEL----------CAARVSE---VLQNRVHRTEEVKHVDFYAF 354
               ::    | | |    |   :          |:|       | :  |    |  | |||
Db        778 CSQCASSVQGGKKGKSGVSIKLVGAPNWGECSALAKNAPCALPDGYPR----PHGQFYAV 833

Qy        355 S------YYYDLAAGVGLIDA-EKGGSLVVGDFEIAAKYVCRTLETQPQSSPF---SCMD 404
              |      :::|:|  | |  |||     :|   | | ||    ||  ||   |
Db        834 SGFFVVYRFFNLSAEASLDDVLEKG-----REFCDKAWQVART-SVSPQ--PFIEQYCFR 885

Qy        405 LTYVSLLLQEFGFPRSKVLKLTRK---IDNVETSWALG 439
              |:  ||:|        | :| |   | :   :| ||
Db        886 APYIVSLLRE-------GLYITDKQIIIGSGSITWTLG 916


RESULT 15
C86276
7A19.33 protein - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: C86276
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: C86276
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-508 <STO>
A;Cross-references: UNIPROT:Q9XI63; GB:AE005172; NID:g5080800; PIDN:AAD39310.1; GSPDB:GN
C;Genetics:
A;Map position: 1
C;Superfamily: nucleoside triphosphatase chromatin-associated

  Query Match             9.3%;  Score 219;  DB 2;  Length 508;
  Best Local Similarity   22.3%;  Pred. No. 8.3e-10;
  Matches  109;  Conservative   83;  Mismatches  196;  Indels  100;  Gaps   21;

Qy          9 SLRVAKVAYPLGLCVGVFIYVAYIKWHRATATQAFFSITRAAPGARWGQQAHSPLGTAAD 68
              | |   : : :  || : : : :|          :|| |:    |
Db         26 SKRTKSIIFVIVACVTIALGLLFIG----------YSILRSGRNRR-------------- 61

Qy         69 GHEVFYGIMFDAGSTGTRVHVFQFTRPPRETPTLT--HETFKAVK--PGLSAYADDVEKS 124
                 : | :: | ||:|||||| : |      |       | : ::|  ||||||||: |
Db         62 -VSLHYSVIIDGGSSGTRVHVFGY-RIESGKPVFDFGEENYASLKLSPGLSAYADNPEGV 119

Qy        125 AQGIRELLDVAKQDIPFDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASPFLVG 184
              :: : ||:: ||: :     | : : | ||||:|||     :::|   : | ::| |
Db        120 SESVTELVEFAKKRVHKGKLKKSDIRLMATAGMRLLELPVQEQILDVTRRVLRSSGFDFR 179

Qy        185 DDCVSIMNGTDEGVSAWITINFLTGSLKTPGGSSVGMLDLGGGSTQIAFLPRVEGTLQAS 244
              |:  |:::   |      : : :: | |          | :     :: |:     : :
Db        180 DEWASVISEILENFQDLMKV-YMLGLL----------LIMRSVRLEVTFV-----STELV 223

Qy        245 PPGYLTALRMFNRTYKLYSYSYLGLGLMSARLAILGGVEGQPAKD-GKELV-SPCLS--- 299
              | :   |  | :| |||:|:|  |  :|:  :   :    |   |: :|  ||:
Db        224 PSEFSRTLAYGNVSYNLYSHSFLDFGQDAAQEKLSESLYNSAANSTGEGIVPDPCIPKGY 283

Qy        300 ----------PSFKGEWEHAEVTYRVSG------QKAAASLHE---LCAARVSEV----- 335
                       | |  :     | : :|        | | | |     |  :   :
Db        284 ILETNLQKDLPGFLADKGKFTATLQAAGNFSECRSAAFAMLQEEKGKCTYKRCSIGSIFT 343

Qy        336 --LQNRVHRTEEVKHVDFYAFSYYYDLAAGVGLIDAEKGGSLVVGD--FEIAAKYVCRTL 391
                 ||     ||      :|:  | :: |     | :   |    |:  ::  ||
Db        344 PNLQGSFLATE-----NFFHTSKFFGLGEKEWLSEMILAGKRFCGEEWSKLKVKYP---- 394

Qy        392 ETQPQSSPFSCMDLTY-VSLLLQEFGFP-RSKVLKLTRKI--DNVETSWALGAI------ 441
                : ::    |    | :|:|    |      : :|   |   :::   |||||
Db        395 TFKDENLLRYCFSSAYIISMLHDSLGVALDDERIKYASKAGEEDIPLDWALGAFILNTAT 454

Qy        442 --FHYIDS 447
                | | |:
Db        455 ATFDYSDN 462


Search completed: November 16, 2004, 17:00:26
Job time : 44 secs
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: November 16, 2004, 16:34:13 ; Search time 196 Seconds
(without alignments)
1338.627 Million cell updates/sec

Title: US-09-905-589A-2
Perfect score: 2364
Sequence: 1 MRKISNHGSLRVAKVAYPLG.....ALGAIFHYIDSLNRQKSPAS 456

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2361	99.9	484	1	ENP6_HUMAN	O75354 homo sapien
2	2361	99.9	503	2	Q8N3H3	Q8n3h3 homo sapien
3	2063.5	87.3	455	1	ENP6_RAT	Q9er31 rattus norv
4	1943	82.2	445	2	Q6YHK4	Q6yhk4 cavia porce
5	1943	82.2	445	2	AAN72326	Aan72326 cavia por
6	1229.5	52.0	278	2	Q8CHZ3	Q8chz3 mus musculu
7	1021	43.2	427	2	Q6P6S9	Q6p6s9 rattus norv
8	1021	43.2	427	2	AAH62044	Aah62044 rattus no
9	1007	42.6	427	1	ENP5_MOUSE	Q9wuz9 mus musculu
10	1007	42.6	427	2	Q8CD29	Q8cd29 mus musculu
11	1007	42.6	427	2	AAK82949	Aak82949 mus muscu
12	1007	42.6	427	2	BAC29515	Bac29515 mus muscu
13	1007	42.6	427	2	BAC29861	Bac29861 mus muscu
14	1007	42.6	427	2	BAC37592	Bac37592 mus muscu
15	1007	42.6	427	2	BAC37862	Bac37862 mus muscu
16	1007	42.6	427	2	BAC38219	Bac38219 mus muscu
17	1007	42.6	427	2	BAC40362	Bac40362 mus muscu
18	1000	42.3	427	2	Q8BR23	Q8br23 mus musculu
19	999	42.3	428	1	ENP5_HUMAN	O75356 homo sapien
20	992	42.0	428	2	Q96RX0	Q96rx0 homo sapien
21	959	40.6	469	1	ENP5_MESAU	Q9qyc8 mesocricetu
22	957	40.5	224	2	Q8CDB6	Q8cdb6 mus musculu
23	636.5	26.9	533	2	Q7PVI8	Q7pvi8 anopheles g
24	621	26.3	461	2	O76268	O76268 drosophila
25	621	26.3	464	2	Q9VQI8	Q9vqi8 drosophila
26	590.5	25.0	479	2	Q9XU84	Q9xu84 caenorhabdi
27	532.5	22.5	595	2	Q6BU56	Q6bu56 debaryomyce
28	531.5	22.5	522	1	GDA1_KLULA	Q9hem6 kluyveromyc
29	528	22.3	489	2	Q8H7L6	Q8h7l6 oryza sativ
30	525.5	22.2	467	2	Q9SPM7	Q9spm7 dolichos bi
31	509	21.5	455	2	Q84UE0	Q84ue0 medicago tr
32	508	21.5	556	1	GDA1_SCHPO	Q9ut35 schizosacch
33	506	21.4	462	2	Q9XFC9	Q9xfc9 dolichos bi
34	505.5	21.4	467	2	Q84UD8	Q84ud8 medicago tr
35	504.5	21.3	467	2	Q8RVT6	Q8rvt6 pisum sativ
36	501.5	21.2	447	2	Q9FUI1	Q9fui1 pisum sativ
37	501	21.2	455	2	Q9SPM6	Q9spm6 medicago sa
38	500	21.2	539	2	Q6CBK6	Q6cbk6 yarrowia li
39	498.5	21.1	541	2	Q6FLR7	Q6flr7 candida gla
40	498	21.1	518	1	GDA1_YEAST	P32621 saccharomyc
41	495	20.9	467	2	Q6Z4P2	Q6z4p2 oryza sativ
42	495	20.9	467	2	BAC83798	Bac83798 oryza sat
43	490	20.7	510	2	Q753F2	Q753f2 ashbya goss
44	490	20.7	510	2	AAS53733	Aas53733 ashbya go
45	489.5	20.7	471	2	Q9SQG2	Q9sqg2 arabidopsis

ALIGNMENTS

RESULT 1
ENP6_HUMAN
ID ENP6_HUMAN STANDARD; PRT; 484 AA.
AC O75354; Q7Z5B5; Q8TAS7; Q9UJD1;
DT 16-OCT-2001 (Rel. 40, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ectonucleoside triphosphate diphosphohydrolase 6 (EC 3.6.1.6)
DE (NTPDase6) (CD39 antigen-like 2).
GN Name=ENTPD6; Synonyms=CD39L2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND VARIANT VAL-138.
RC TISSUE=Keratinocytes;
RX MEDLINE=98341119; PubMed=9676430;
RA Chadwick B.P., Frischauf A.-M.;
RT "The CD39-like gene family: identification of three new human members
RT (CD39L2, CD39L3, and CD39L4), their murine homologues, and a member of
RT the gene family from Drosophila melanogaster.";
RL Genomics 50:357-367(1998).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21638749; PubMed=11780052; DOI=10.1038/414865a;
RA Deloukas P., Matthews L.H., Ashurst J.L., Burton J., Gilbert J.G.R.,
RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,
RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,
RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA Lehvaeslaiho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
RA Marsh V.L., Martin S.L., McConnachie L.J., McLay K., McMurray A.A.,
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Shownkeen R., Sims S.,
RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RA Rogers J.;
RT "The DNA sequence and comparative analysis of human chromosome 20.";
RL Nature 414:865-871(2001).
RN [3]

```
RP   SEQUENCE FROM N.A., AND SOLUBLE FORM DISULFIDE BONDS.
RX   PubMed=14529283; DOI=10.1021/bi035137r;
RA   Ivanenkov V.V., Murphy-Piedmonte D.M., Kirley T.L.;
RT   "Bacterial expression, characterization, and disulfide bond
RT   determination of soluble human NTPDase6 (CD39L2) nucleotidase:
RT   implications for structure and function.";
RL   Biochemistry 42:11726-11735(2003).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Placenta;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [5]
RP   SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY.
RX   PubMed=11041856; DOI=10.1021/bi000959z;
RA   Yeung G., Mulero J.J., McGowan D.W., Bajwa S.S., Ford J.E.;
RT   "CD39L2, a gene encoding a human nucleoside diphosphatase,
RT   predominantly expressed in the heart.";
RL   Biochemistry 39:12916-12923(2000).
CC   -!- FUNCTION: Might support glycosylation reactions in the Golgi
CC       apparatus and, when released from cells, might catalyze the
CC       hydrolysis of extracellular nucleotides. Hydrolyzes preferentially
CC       nucleoside 5'-diphosphates, nucleoside 5'-triphosphates are
CC       hydrolyzed only to a minor extent, there is no hydrolysis of
CC       nucleoside 5'-monophosphates. The order of activity with different
CC       substrates is GDP > IDP >> UDP = CDP >> ADP (By similarity).
CC   -!- CATALYTIC ACTIVITY: A nucleoside diphosphate + H(2)O = a
CC       nucleotide + phosphate.
CC   -!- COFACTOR: Requires calcium and magnesium (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type II membrane protein. Golgi. But also
CC       occurs in a soluble extracellular form.
CC   -!- TISSUE SPECIFICITY: Expressed in most tissues, but predominantly
CC       in heart.
CC   -!- SIMILARITY: Belongs to the GDA1 / CD39 NTPase family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF039916; AAC39883.1; -.
DR   EMBL; AL035252; CAB41571.1; -.
DR   EMBL; AY327581; AAP92131.1; -.
DR   EMBL; BC025980; AAH25980.1; -.
DR   Genew; HGNC:3368; ENTPD6.
DR   MIM; 603160; -.
DR   InterPro; IPR000407; GDA1_CD39_NTPase.
DR   Pfam; PF01150; GDA1_CD39; 1.
DR   PROSITE; PS01238; GDA1_CD39_NTPASE; FALSE_NEG.
KW   Calcium; Glycoprotein; Golgi stack; Hydrolase; Magnesium;
KW   Polymorphism; Signal-anchor; Transmembrane.
```

```
FT   DOMAIN        1     39       Cytoplasmic (Potential).
FT   TRANSMEM     40     60       Signal-anchor for type II membrane
FT                                protein (Potential).
FT   DOMAIN       61    484       Lumenal (Potential).
FT   DISULFID    325    356       In soluble form.
FT   DISULFID    416    430       In soluble form.
FT   CARBOHYD    220    220       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    284    284       N-linked (GlcNAc. . .) (Potential).
FT   VARIANT     138    138       L -> V (in dbSNP:1044567).
FT                                /FTId=VAR_017863.
FT   CONFLICT     14     14       S -> N (in Ref. 3).
FT   CONFLICT     19     19       Missing (in Ref. 4).
FT   CONFLICT    202    202       E -> K (in Ref. 2).
SQ   SEQUENCE   484 AA;  53247 MW;  604C958953179089 CRC64;
```

```
  Query Match           99.9%;  Score 2361;  DB 1;  Length 484;
  Best Local Similarity 99.8%;  Pred. No. 1.6e-177;
  Matches  455;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRKISNHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRATATQAFFSITRAAPGARWGQQAH 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         29 MRKISNHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRATATQAFFSITRAAPGARWGQQAH 88

Qy         61 SPLGTAADGHEVFYGIMFDAGSTGTRVHVFQFTRPPRETPTLTHETFKAVKPGLSAYADD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||:||||||||||
Db         89 SPLGTAADGHEVFYGIMFDAGSTGTRVHVFQFTRPPRETPTLTHETFKALKPGLSAYADD 148

Qy        121 VEKSAQGIRELLDVAKQDIPFDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASP 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        149 VEKSAQGIRELLDVAKQDIPFDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASP 208

Qy        181 FLVGDDCVSIMNGTDEGVSAWITINFLTGSLKTPGGSSVGMLDLGGGSTQIAFLPRVEGT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        209 FLVGDDCVSIMNGTDEGVSAWITINFLTGSLKTPGGSSVGMLDLGGGSTQIAFLPRVEGT 268

Qy        241 LQASPPGYLTALRMFNRTYKLYSYSYLGLGLMSARLAILGGVEGQPAKDGKELVSPCLSP 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        269 LQASPPGYLTALRMFNRTYKLYSYSYLGLGLMSARLAILGGVEGQPAKDGKELVSPCLSP 328

Qy        301 SFKGEWEHAEVTYRVSGQKAAASLHELCAARVSEVLQNRVHRTEEVKHVDFYAFSYYYDL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        329 SFKGEWEHAEVTYRVSGQKAAASLHELCAARVSEVLQNRVHRTEEVKHVDFYAFSYYYDL 388

Qy        361 AAGVGLIDAEKGGSLVVGDFEIAAKYVCRTLETQPQSSPFSCMDLTYVSLLLQEFGFPRS 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        389 AAGVGLIDAEKGGSLVVGDFEIAAKYVCRTLETQPQSSPFSCMDLTYVSLLLQEFGFPRS 448

Qy        421 KVLKLTRKIDNVETSWALGAIFHYIDSLNRQKSPAS 456
              ||||||||||||||||||||||||||||||||||||
Db        449 KVLKLTRKIDNVETSWALGAIFHYIDSLNRQKSPAS 484
```

```
RESULT 2
Q8N3H3
ID   Q8N3H3      PRELIMINARY;      PRT;   503 AA.
AC   Q8N3H3;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hypothetical protein DKFZp761J1915 (Fragment).
GN   Name=DKFZp761J1915;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Amygdala;
RA   Ansorge W., Wirkner U., Mewes H.W., Weil B., Wiemann S.;
RL   Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AL834158; CAD38864.1; -.
DR   GO; GO:0016787; F:hydrolase activity; IEA.
DR   InterPro; IPR000407; GDA1_CD39_NTPase.
```

```
DR   Pfam; PF01150; GDA1_CD39; 1.
KW   Hypothetical protein.
FT   NON_TER       1       1
SQ   SEQUENCE   503 AA;  54763 MW;  163933F9139D8D9F CRC64;

  Query Match             99.9%;  Score 2361;  DB 2;  Length 503;
  Best Local Similarity   99.8%;  Pred. No. 1.7e-177;
  Matches  455;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRKISNHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRATATQAFFSITRAAPGARWGQQAH 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         48 MRKISNHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRATATQAFFSITRAAPGARWGQQAH 107

Qy         61 SPLGTAADGHEVFYGIMFDAGSTGTRVHVFQFTRPPRETPTLTHETFKAVKPGLSAYADD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||:||||||||||
Db        108 SPLGTAADGHEVFYGIMFDAGSTGTRVHVFQFTRPPRETPTLTHETFKALKPGLSAYADD 167

Qy        121 VEKSAQGIRELLDVAKQDIPFDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASP 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        168 VEKSAQGIRELLDVAKQDIPFDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASP 227

Qy        181 FLVGDDCVSIMNGTDEGVSAWITINFLTGSLKTPGGSSVGMLDLGGGSTQIAFLPRVEGT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        228 FLVGDDCVSIMNGTDEGVSAWITINFLTGSLKTPGGSSVGMLDLGGGSTQIAFLPRVEGT 287

Qy        241 LQASPPGYLTALRMFNRTYKLYSYSYLGLGLMSARLAILGGVEGQPAKDGKELVSPCLSP 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        288 LQASPPGYLTALRMFNRTYKLYSYSYLGLGLMSARLAILGGVEGQPAKDGKELVSPCLSP 347

Qy        301 SFKGEWEHAEVTYRVSGQKAAASLHELCAARVSEVLQNRVHRTEEVKHVDFYAFSYYYDL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        348 SFKGEWEHAEVTYRVSGQKAAASLHELCAARVSEVLQNRVHRTEEVKHVDFYAFSYYYDL 407

Qy        361 AAGVGLIDAEKGGSLVVGDFEIAAKYVCRTLETQPQSSPFSCMDLTYVSLLLQEFGFPRS 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        408 AAGVGLIDAEKGGSLVVGDFEIAAKYVCRTLETQPQSSPFSCMDLTYVSLLLQEFGFPRS 467

Qy        421 KVLKLTRKIDNVETSWALGAIFHYIDSLNRQKSPAS 456
              ||||||||||||||||||||||||||||||||||||
Db        468 KVLKLTRKIDNVETSWALGAIFHYIDSLNRQKSPAS 503


RESULT 3
ENP6_RAT
ID   ENP6_RAT       STANDARD;      PRT;   455 AA.
AC   Q9ER31;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Ectonucleoside triphosphate diphosphohydrolase 6 (EC 3.6.1.6)
DE   (NTPDase6) (CD39 antigen-like 2).
GN   Name=Entpd6; Synonyms=Cd39l2;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A., SUBCELLULAR LOCATION, AND CHARACTERIZATION.
RC   STRAIN=Sprague-Dawley; TISSUE=Brain;
RX   MEDLINE=20498744; PubMed=11042118;
RA   Braun N., Fengler S., Ebeling C., Servos J., Zimmermann H.;
RT   "Sequencing, functional expression and characterization of rat
RT   NTPDase6, a nucleoside diphosphatase and novel member of the ecto-
RT   nucleoside triphosphate diphosphohydrolase family.";
RL   Biochem. J. 351:639-647(2000).
CC   -!- FUNCTION: Might support glycosylation reactions in the Golgi
CC       apparatus and, when released from cells, might catalyze the
CC       hydrolysis of extracellular nucleotides. Hydrolyzes preferentially
CC       nucleoside 5'-diphosphates, nucleoside 5'-triphosphates are
CC       hydrolyzed only to a minor extent, there is no hydrolysis of
CC       nucleoside 5'-monophosphates. The order of activity with different
CC       substrates is GDP > IDP >> UDP = CDP >> ADP.
CC   -!- CATALYTIC ACTIVITY: A nucleoside diphosphate + H(2)O = a
CC       nucleotide + phosphate.
CC   -!- COFACTOR: Requires calcium and magnesium.
CC   -!- SUBCELLULAR LOCATION: Type II membrane protein. Golgi. But also
CC       occurs in a soluble extracellular form.
CC   -!- SIMILARITY: Belongs to the GDA1 / CD39 NTPase family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AJ277748; CAC16598.1; -.
DR   RGD; 619725; Entpd6.
DR   InterPro; IPR000407; GDA1_CD39_NTPase.
DR   Pfam; PF01150; GDA1_CD39; 1.
DR   PROSITE; PS01238; GDA1_CD39_NTPASE; FALSE_NEG.
KW   Calcium; Glycoprotein; Golgi stack; Hydrolase; Magnesium;
KW   Signal-anchor; Transmembrane.
FT   DOMAIN        1     12       Cytoplasmic (Potential).
FT   TRANSMEM     13     32       Signal-anchor for type II membrane
FT                                protein (Potential).
FT   DOMAIN       33    455       Lumenal (Potential).
FT   DISULFID    297    327       In soluble form (By similarity).
FT   DISULFID    387    401       In soluble form (By similarity).
FT   CARBOHYD    192    192       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    256    256       N-linked (GlcNAc. . .) (Potential).
SQ   SEQUENCE   455 AA;  49899 MW;  19A22E8BAEF0F77B CRC64;

  Query Match             87.3%;  Score 2063.5;  DB 1;  Length 455;
  Best Local Similarity   86.6%;  Pred. No. 4.3e-154;
  Matches  394;  Conservative   27;  Mismatches   33;  Indels    1;  Gaps    1;

Qy          1 MRKISNHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRATATQAFFSITRAAPGARWGQQAH 60
              |||| |||:||: ||||||||||||:||||||||||||:| ||||:|  || | || |||
Db          1 MRKIPNHGTLRMTKVAYPLGLCVGLFIYVAYIKWHRASAAQAFFTIAGAASGVRWTQQAF 60

Qy         61 SPLGTAADGHEVFYGIMFDAGSTGTRVHVFQFTRPPRETPTLTHETFKAVKPGLSAYADD 120
              |   :|  ||||||||||||||||||:||||| ||| ||||||||||||:||||||||||
Db         61 SSPDSATRGHEVFYGIMFDAGSTGTRIHVFQFARPPGETPTLTHETFKALKPGLSAYADD 120

Qy        121 VEKSAQGIRELLDVAKQDIPFDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASP 180
              ||||||||:|||:|||| ||:|||||||||||||||||||||||||||||||||||||||
Db        121 VEKSAQGIQELLNVAKQHIPYDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASP 180

Qy        181 FLVGDDCVSIMNGTDEGVSAWITINFLTGSLKTPGGSSVGMLDLGGGSTQIAFLPRVEGT 240
              ||||||||||||||||||:|||||||||| ||||||||||||| ||||||||
Db        181 FLVGDDCVSIMNGTDEGVSAWITVNFLTGSLKTPGSSSVGMLDLGGGSTQITFLPRVEGT 240

Qy        241 LQASPPGYLTALRMFNRTYKLYSYSYLGLGLMSARLAILGGVEGQPAKDGKELVSPCLSP 300
              |||||||:||||:|||||:|||||||||||||||||||||||||:||:| ||||||||||
Db        241 LQASPPGHLTALQMFNRTFKLYSYSYLGLGLMSARLAILGGVEGKPAEDDKELVSPCLSP 300

Qy        301 SFKGEWEHAEVTYRVSGQKAAASLHELCAARVSEVLQNRVHRTEEVKHVDFYAFSYYYDL 360
              |:|:||||||||:|||| |  |:||||:||||||:|:|||||| :|||||||||||||||
Db        301 RFRGKWEHAEVTYRISGQK-AVGLYELCASRVSEVLRNKVHRTEEAQHVDFYAFSYYYDL 359

Qy        361 AAGVGLIDAEKGGSLVVGDFEIAAKYVCRTLETQPQSSPFSCMDLTYVSLLLQEFGFPRS 420
              ||  ||||||||||||||||||||||||||||||| ||||:||||||:|||| |||||
Db        360 AASFGLIDAEKGGSLVVGDFEIAAKYVCRTLETQPPSSPFACMDLTYISLLLHEFGFPGD 419

Qy        421 KVLKLTRKIDNVETSWALGAIFHYIDSLNRQKSPA 455
              ||||| |||||||||||||||||||| || ||
Db        420 KVLKLARKIDNVETSWALGAIFHYIDSLKRQKVPA 454


RESULT 4
Q6YHK4
ID   Q6YHK4       PRELIMINARY;      PRT;   445 AA.
AC   Q6YHK4;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
```

```
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Ectonucleoside triphosphate diphosphohydrolase 6.
OS   Cavia porcellus (Guinea pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX   NCBI_TaxID=10141;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RA   Mihaylova-Todorova S.T., Choe S.M., Miller L.J., Horowitz B.,
RA   Westfall D.P.;
RL   Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY149906; AAN72326.1; -.
DR   GO; GO:0016787; F:hydrolase activity; IEA.
DR   InterPro; IPR000407; GDA1_CD39_NTPase.
DR   Pfam; PF01150; GDA1_CD39; 1.
KW   Hydrolase.
SQ   SEQUENCE   445 AA;  48357 MW;  890CEFD068405698 CRC64;

  Query Match             82.2%;  Score 1943;  DB 2;  Length 445;
  Best Local Similarity   82.9%;  Pred. No. 1.4e-144;
  Matches  377;  Conservative   31;  Mismatches   37;  Indels   10;  Gaps    3;

Qy          1 MRKISNHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRATATQAFFSITRAAPGARWGQQAH 60
              |||| :|||||: :||| ||||||:|||||||||:|:| |   ||    |||     ||
Db          1 MRKIPSHGSLRMTRVAYLLGLCVGLFIYVAYIKWHQASAPQVLSSI----PGA-----AH 51

Qy         61 SPLGTAADGHEVFYGIMFDAGSTGTRVHVFQFTRPPRETPTLTHETFKAVKPGLSAYADD 120
              |:|:||   |||||||||||||||||||||| ||| ||||||||||:||||||||||
Db         52 IPVGSAAHALEVFYGIMFDAGSTGTRVHVFQFARPPGETPTLTHETFKALKPGLSAYADD 111

Qy        121 VEKSAQGIRELLDVAKQDIPFDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASP 180
              ||||||||:|||||||||||||||||||||||||||||||||||:||||||||||||
Db        112 VEKSAQGIQELLDVAKQDIPFDFWKATPLVLKATAGLRLLPGEKAQRLLQKVKEVFKASP 171

Qy        181 FLVGDDCVSIMNGTDEGVSAWITINFLTGSLKTPGGSSVGMLDLGGGSTQIAFLPRVEGT 240
              ||||:|||||||||||||||||||||||||: || |||||||||||||| |||| :||
Db        172 FLVGEDCVSIMNGTDEGVSAWITINFLTGSLRAPGRSSVGMLDLGGGSTQITFLPRAKGT 231

Qy        241 LQASPPGYLTALRMFNRTYKLYSYSYLGLGLMSARLAILGGVEGQPAKDGKELVSPCLSP 300
              |:|||||:||:|:||||||:|||:|||||||||||||||||||:||||||||||||||
Db        232 LEASPPGHLTSLQMFNRTYRLYSHSYLGLGLMSARLAILGGVEGRPAKDGKELVSPCLSP 291

Qy        301 SFKGEWEHAEVTYRVSGQKAAASLHELCAARVSEVLQNRVHRTEEVKHVDFYAFSYYYDL 360
              |:|||||| :|||:|| | |  ||| ||:|||||||::||| ||  ||||||||||||
Db        292 GFRGEWEHAGITYRISGPK-AGRLHEPCASRVSEVLQSKVHRAEEAGHVDFYAFSYYYDL 350

Qy        361 AAGVGLIDAEKGGSLVVGDFEIAAKYVCRTLETQPQSSPFSCMDLTYVSLLLQEFGFPRS 420
              || |||||||||||: : ||||||||||||  ||  ||| ||||||||||:|||||
Db        351 AASVGLIDAEKGGSVSLEDFEIAAKYVCRTLGAQPHHSPFLCMDLTYVSLLLREFGFPGD 410

Qy        421 KVLKLTRKIDNVETSWALGAIFHYIDSLNRQKSPA 455
              |||||||||||||||||||||||||:|||||| |
Db        411 KVLKLTRKIDNVETSWALGAIFHYIDALNRQKSAA 445


RESULT 5
AAN72326
ID   AAN72326     PRELIMINARY;      PRT;   445 AA.
AC   AAN72326;
DT   02-MAR-2004 (TrEMBLrel. 27, Created)
DT   02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT   02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE   Ectonucleoside triphosphate diphosphohydrolase 6.
OS   Cavia porcellus (Guinea pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX   NCBI_TaxID=10141;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RA   Mihaylova-Todorova S.T., Choe S.M., Miller L.J., Horowitz B.,
RA   Westfall D.P.;
RT   "Sequencing of an ectonucleoside triphosphate diphosphohydrolase
RT   homolog of NTPDase6 from guinea pig.";
RL   Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY149906; AAN72326.1; -.
KW   Hydrolase.
SQ   SEQUENCE   445 AA;  48357 MW;  890CEFD068405698 CRC64;

  Query Match             82.2%;  Score 1943;  DB 2;  Length 445;
  Best Local Similarity   82.9%;  Pred. No. 1.4e-144;
  Matches  377;  Conservative   31;  Mismatches   37;  Indels   10;  Gaps    3;

Qy          1 MRKISNHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRATATQAFFSITRAAPGARWGQQAH 60
              |||| :|||||: :||| ||||||:|||||||||:|:| |   ||    |||     ||
Db          1 MRKIPSHGSLRMTRVAYLLGLCVGLFIYVAYIKWHQASAPQVLSSI----PGA-----AH 51

Qy         61 SPLGTAADGHEVFYGIMFDAGSTGTRVHVFQFTRPPRETPTLTHETFKAVKPGLSAYADD 120
              |:|:||   |||||||||||||||||||||| ||| ||||||||||:||||||||||
Db         52 IPVGSAAHALEVFYGIMFDAGSTGTRVHVFQFARPPGETPTLTHETFKALKPGLSAYADD 111

Qy        121 VEKSAQGIRELLDVAKQDIPFDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASP 180
              ||||||||:|||||||||||||||||||||||||||||||||||:||||||||||||
Db        112 VEKSAQGIQELLDVAKQDIPFDFWKATPLVLKATAGLRLLPGEKAQRLLQKVKEVFKASP 171

Qy        181 FLVGDDCVSIMNGTDEGVSAWITINFLTGSLKTPGGSSVGMLDLGGGSTQIAFLPRVEGT 240
              ||||:|||||||||||||||||||||||||: || |||||||||||||| |||| :||
Db        172 FLVGEDCVSIMNGTDEGVSAWITINFLTGSLRAPGRSSVGMLDLGGGSTQITFLPRAKGT 231

Qy        241 LQASPPGYLTALRMFNRTYKLYSYSYLGLGLMSARLAILGGVEGQPAKDGKELVSPCLSP 300
              |:|||||:||:|:||||||:|||:|||||||||||||||||||:||||||||||||||
Db        232 LEASPPGHLTSLQMFNRTYRLYSHSYLGLGLMSARLAILGGVEGRPAKDGKELVSPCLSP 291

Qy        301 SFKGEWEHAEVTYRVSGQKAAASLHELCAARVSEVLQNRVHRTEEVKHVDFYAFSYYYDL 360
              |:|||||| :|||:|| | |  ||| ||:|||||||::||| ||  ||||||||||||
Db        292 GFRGEWEHAGITYRISGPK-AGRLHEPCASRVSEVLQSKVHRAEEAGHVDFYAFSYYYDL 350

Qy        361 AAGVGLIDAEKGGSLVVGDFEIAAKYVCRTLETQPQSSPFSCMDLTYVSLLLQEFGFPRS 420
              || |||||||||||: : ||||||||||||  ||  ||| ||||||||||:|||||
Db        351 AASVGLIDAEKGGSVSLEDFEIAAKYVCRTLGAQPHHSPFLCMDLTYVSLLLREFGFPGD 410

Qy        421 KVLKLTRKIDNVETSWALGAIFHYIDSLNRQKSPA 455
              |||||||||||||||||||||||||:|||||| |
Db        411 KVLKLTRKIDNVETSWALGAIFHYIDALNRQKSAA 445


RESULT 6
Q8CHZ3
ID   Q8CHZ3      PRELIMINARY;      PRT;   278 AA.
AC   Q8CHZ3;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Ectonucleoside triphosphate diphosphohydrolase 6.
GN   Name=Entpd6;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Mammary gland;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
```

```
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Mammary gland;
RA   Strausberg R.;
RL   Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC038126; AAH38126.1; -.
DR   MGD; MGI:1202295; Entpd6.
DR   GO; GO:0016787; F:hydrolase activity; IEA.
DR   InterPro; IPR000407; GDA1_CD39_NTPase.
DR   Pfam; PF01150; GDA1_CD39; 1.
KW   Hydrolase.
SQ   SEQUENCE   278 AA;  30130 MW;  75A92DD1AC76297F CRC64;

  Query Match             52.0%;  Score 1229.5;  DB 2;  Length 278;
  Best Local Similarity   85.6%;  Pred. No. 1.4e-88;
  Matches  237;  Conservative   17;  Mismatches   18;  Indels    5;  Gaps    1;

Qy          1 MRKISNHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRATATQAFFSITRAAPGARWGQQAH 60
              |||| |||:|:|: |||||||||||:|||||||||||:| ||||:|  || |||| |||
Db          1 MRKIPNHGTLRMTKVAYPLGLCVGLFIYVAYIKWHRASAAQAFFTIAGAASGARWTQQAF 60

Qy         61 SPLGTAADGHEVFYGIMFDAGSTGTRVHVFQFTRPPRETPTLTHETFKAVKPGLSAYADD 120
              |  |:|| |||||||||||||||||:||||| ||| ||||||||||||:||||||||||
Db         61 SSPGSAARGHEVFYGIMFDAGSTGTRIHVFQFARPPGETPTLTHETFKALKPGLSAYADD 120

Qy        121 VEKSAQGIRELLDVAKQDIPFDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASP 180
              |||||||:|||:|||| ||:|||||||||||||||||||||||||||||||||||||||
Db        121 VEKSAQGIQELLNVAKQHIPYDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASP 180

Qy        181 FLVGDDCVSIMNGTDEGVSAWITINFLTGSLKTPGGSSVGMLDLGGGSTQIAFLPRVEGT 240
              |||||||||||||||||||:||||||||||  |||||||||||||  ||||||||
Db        181 FLVGDDCVSIMNGTDEGVSAWITVNFLTGSLKTPGSSSVGMLDLGGGSTQITFLPRVEGT 240

Qy        241 LQASPPGYLTALRMFNRTYKLYSYSYLGLGLMSARLA 277
              |||||||:||||:||||||||||| :     : :|||
Db        241 LQASPPGHLTALQMFNRTYKLYSYRW-----VCSRLA 272


RESULT 7
Q6P6S9
ID   Q6P6S9      PRELIMINARY;      PRT;   427 AA.
AC   Q6P6S9;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Ectonucleoside triphosphate diphosphohydrolase 5.
GN   Name=Entpd5;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Prostate;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Prostate;
RA   Strausberg R.;
RL   Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC062044; AAH62044.1; -.
DR   GO; GO:0016787; F:hydrolase activity; IEA.
DR   InterPro; IPR000407; GDA1_CD39_NTPase.
DR   Pfam; PF01150; GDA1_CD39; 1.
KW   Hydrolase.
SQ   SEQUENCE   427 AA;  47372 MW;  6CBBC44D96A60211 CRC64;

  Query Match             43.2%;  Score 1021;  DB 2;  Length 427;
  Best Local Similarity   53.2%;  Pred. No. 6.9e-72;
  Matches  207;  Conservative   58;  Mismatches  118;  Indels    6;  Gaps    4;

Qy         62 PLGTAADGHEVFYGIMFDAGSTGTRVHVFQFT-RPPRETPTLTHETFKAVKPGLSAYADD 120
              |:  :|      |||||||||||||:||: |   |    :  | |  | | :|||||||: |
Db         39 PVNVSAG---TFYGIMFDAGSTGTRIHVYTFVQRTSGQLPFLEGEIFDSVKPGLSAFVDQ 95

Qy        121 VEKSAQGIRELLDVAKQDIPFDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASP 180
              :: |: ::|||:|||   ||   || ||:||||||||||| :||| || :|:|:|| ||
Db         96 PKQGAETVQELLEVAKDSIPRSHWKRTPVVLKATAGLRLLPEQKAQTLLLEVEEIFKNSP 155

Qy        181 FLVGDDCVSIMNGTDEGVSAWITINFLTGSLKTPGGSSVGMLDLGGGSTQIAFLPRVEGT 240
              ||| || ||||:|: ||: ||:|:|||||  |   |  :|| ||||| |||| |||::| |
Db        156 FLVPDDSVSIMDGSYEGILAWVTVNFLTGQLHGRGQETVGTLDLGGASTQITFLPQLEKT 215

Qy        241 LQASPPGYLTALRMFNRTYKLYSYSYLGLGLMSARLAILGGVEGQPAKDGKELVSPCLSP 300
              |: :| ||| :  ||| |:|||::|||| || :|||| || :| :   ||    | ||
Db        216 LEQTPKGYLASFEMFNSTFKLYTHSYLGFGLKAARLATLGALEAE-GTDGHTFRSACLPR 274

Qy        301 SFKGEWEHAEVTYRVSGQKAAASLHELCAARVSEVLQNRVHRTEEVKHVDFYAFSYYYDL 360
              : ||    | |:  | :       | | | |  |:| ::|: ||::   |||||||||
Db        275 WLEAEWIFGGVKYQYGGNQEGEMGFEPCYAEVRRVVQGKLHQPEEIRGSSFYAFSYYYDR 334

Qy        361 AAGVGLIDAEKGGSLVVGDFEIAAKYVCRTLETQPQSSPFSCMDLTYVSLLLQE-FGFPR 419
              ||   ||| |||| | | |||  |: ||  ||:    ||| ||||:|:: ||:: |||
Db        335 AAETHLIDYEKGGVLKVEDFERKAREVCDNLESFSSGSPFLCMDLSYITALLKDGFGFED 394

Qy        420 SKVLKLTRKIDNVETSWALGAIFHYIDSL 448
              :|:||:|::|:|| ||||| || : ||
Db        395 GTLLQLTKKVNNIETGWALGATFHLLQSL 423


RESULT 8
AAH62044
ID   AAH62044    PRELIMINARY;      PRT;   427 AA.
AC   AAH62044;
DT   02-MAR-2004 (TrEMBLrel. 27, Created)
DT   02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT   02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE   Ectonucleoside triphosphate diphosphohydrolase 5.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Prostate;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
```

```
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Prostate;
RA   Strausberg R.;
RL   Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC062044; AAH62044.1; -.
KW   Hydrolase.
SQ   SEQUENCE   427 AA;  47372 MW;  6CBBC44D96A60211 CRC64;

  Query Match             43.2%;  Score 1021;  DB 2;  Length 427;
  Best Local Similarity   53.2%;  Pred. No. 6.9e-72;
  Matches  207;  Conservative   58;  Mismatches  118;  Indels    6;  Gaps    4;

Qy         62 PLGTAADGHEVFYGIMFDAGSTGTRVHVFQFT-RPPRETPTLTHETFKAVKPGLSAYADD 120
              |:  :|     |||||||||||||:||: |   |    : | |   | | :|||||||: |
Db         39 PVNVSAG---TFYGIMFDAGSTGTRIHVYTFVQRTSGQLPFLEGEIFDSVKPGLSAFVDQ 95

Qy        121 VEKSAQGIRELLDVAKQDIPFDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASP 180
               :: |: ::|||:|||   ||    || ||:|||||||||||| :||| || :|:|:|| ||
Db         96 PKQGAETVQELLEVAKDSIPRSHWKRTPVVLKATAGLRLLPEQKAQTLLLEVEEIFKNSP 155

Qy        181 FLVGDDCVSIMNGTDEGVSAWITINFLTGSLKTPGGSSVGMLDLGGGSTQIAFLPRVEGT 240
              ||| || ||||:|: ||: ||:|:|||| |    |  :|| ||||| |||| |||::| |
Db        156 FLVPDDSVSIMDGSYEGILAWVTVNFLTGQLHGRGQETVGTLDLGGASTQITFLPQLEKT 215

Qy        241 LQASPPGYLTALRMFNRTYKLYSYSYLGLGLMSARLAILGGVEGQPAKDGKELVSPCLSP 300
              |: :| ||| :  ||| |:|||::|||| || :|||| || :| :   ||    | ||
Db        216 LEQTPKGYLASPEMFNSTFKLYTHSYLGFGLKAARLATLGALEAE-GTDGHTFRSACLPR 274

Qy        301 SFKGEWEHAEVTYRVSGQKAAASLHELCAARVSEVLQNRVHRTEEVKHVDFYAFSYYYDL 360
               : ||    | |:  | :       | | | |  |:| ::|: ||::   |||||||||
Db        275 WLEAEWIFGGVKYQYGGNQEGEMGFEPCYAEVRRVVQGKLHQPEEIRGSSFYAFSYYYDR 334

Qy        361 AAGVGLIDAEKGGSLVVGDFEIAAKYVCRTLETQPQSSPFSCMDLTYVSLLLQE-FGFPR 419
              ||   ||| |||| | | |||  |: ||  ||:    ||| ||||:|:: ||:: |||
Db        335 AAETHLIDYEKGGVLKVEDFERKAREVCDNLESFSSGSPFLCMDLSYITALLKDGFGFED 394

Qy        420 SKVLKLTRKIDNVETSWALGAIFHYIDSL 448
               :|:||:|::|:|| ||||| || : ||
Db        395 GTLLQLTKKVNNIETGWALGATFHLLQSL 423


RESULT 9
ENP5_MOUSE
ID   ENP5_MOUSE     STANDARD;      PRT;   427 AA.
AC   Q9WUZ9; O70214;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Ectonucleoside triphosphate diphosphohydrolase 5 precursor
DE   (EC 3.6.1.6) (NTPDase5) (Nucleoside diphosphatase) (CD39 antigen-like
DE   4) (ER-UDPase).
GN   Name=Entpd5; Synonyms=Cd3914;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Testis;
RX   MEDLINE=98119025; PubMed=9457681;
RA   Chadwick B.P., Williamson J., Sheer D., Frischauf A.-M.;
RT   "cDNA cloning and chromosomal mapping of a mouse gene with homology to
RT   NTPases.";
RL   Mamm. Genome 9:162-164(1998).
RN   [2]
RP   SEQUENCE FROM N.A., SUBCELLULAR LOCATION, AND CHARACTERIZATION.
RC   TISSUE=Liver;
RX   MEDLINE=99298181; PubMed=10369669;
RA   Trombetta E.S., Helenius A.;
RT   "Glycoprotein reglucosylation and nucleotide sugar utilization in the
RT   secretory pathway: identification of a nucleoside diphosphatase in the
RT   endoplasmic reticulum.";
RL   EMBO J. 18:3282-3292(1999).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Kidney;
RX   MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA   Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA   Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA   Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA   Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA   Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA   Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA   Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA   Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA   Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA   Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA   Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA   Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA   Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA   Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA   Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA   Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA   Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA   Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA   Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA   Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA   Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA   Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA   Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA   Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA   Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA   Birney E., Hayashizaki Y.;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=FVB/N; TISSUE=Kidney;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
```

```
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC   -!- FUNCTION: Likely to promote reglycosylation reactions involved in
CC       glycoproteins folding and quality control in the endoplasmic
CC       reticulum. Hydrolyzes UDP, GDP and IDP but not any other
CC       nucleoside di-, mono- or triphosphates, nor thiamine
CC       pyrophosphate.
CC   -!- CATALYTIC ACTIVITY: A nucleoside diphosphate + H(2)O = a
CC       nucleotide + phosphate.
CC   -!- COFACTOR: Requires calcium and magnesium.
CC   -!- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
CC   -!- TISSUE SPECIFICITY: Ubiquitous.
CC   -!- PTM: N-glycosylated; high-mannose type.
CC   -!- MISCELLANEOUS: Optimal pH is neutral.
CC   -!- SIMILARITY: Belongs to the GDA1 / CD39 NTPase family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF006482; AAC05181.1; -.
DR   EMBL; AJ238636; CAB45533.1; -.
DR   EMBL; AK002618; BAB22234.1; -.
DR   EMBL; BC015247; AAH15247.1; -.
DR   MGD; MGI:1321385; Entpd5.
DR   InterPro; IPR000407; GDA1_CD39_NTPase.
DR   Pfam; PF01150; GDA1_CD39; 1.
DR   PROSITE; PS01238; GDA1_CD39_NTPASE; FALSE_NEG.
KW   Calcium; Endoplasmic reticulum; Glycoprotein; Hydrolase; Magnesium;
KW   Signal; Transmembrane.
FT   SIGNAL        1     18       Potential.
FT   CHAIN        19    427       Ectonucleoside triphosphate
FT                                 diphosphohydrolase 5.
FT   CARBOHYD     41     41       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    231    231       N-linked (GlcNAc. . .) (Potential).
FT   CONFLICT    390    390       F -> L (in Ref. 1).
FT   CONFLICT    394    427       DGTLLQLTKKVNNIETGWALGATFHLLQSLGITS -> ERH
FT                                 PLTAHKESEQHRDWLGLGGHLSPAPVSGHHQLRPSSTSEAC
FT                                 ISEPVFSQEGVDSETFSDLSGKAWPETR (in Ref. 1).
SQ   SEQUENCE   427 AA;  47101 MW;  2F9DA2C342C55577 CRC64;

  Query Match             42.6%;  Score 1007;  DB 1;  Length 427;
  Best Local Similarity   50.0%;  Pred. No. 8.8e-71;
  Matches  213;  Conservative   62;  Mismatches  133;  Indels   18;  Gaps    6;

Qy         37 ATATQAFFSITRAAPGA--------RWGQ----QAHSPLGTAADGHEVFYGIMFDAGSTG 84
              ||:  | | :  |  |:          | :     :  |:  :|     ||||||||||||
Db          2 ATSWGAVFMLIIACVGSTVFYREQQTWFEGVFLSSMCPINVSAG---TFYGIMFDAGSTG 58

Qy         85 TRVHVFQFT-RPPRETPTLTHETFKAVKPGLSAYADDVEKSAQGIRELLDVAKQDIPFDF 143
              ||:||:  |   :   : | |  | | :|||||||: |  :: |: ::|||:|||  ||
Db         59 TRIHVYTFVQKTAGQLPFLEGEIFDSVKPGLSAFVDQPKQGAETVQELLEVAKDSIPRSH 118

Qy        144 WKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASPFLVGDDCVSIMNGTDEGVSAWIT 203
              |: ||:|||||||||||| :||| || :|:|:|| ||||| |  ||||:|: ||: ||:|
Db        119 WERTPVVLKATAGLRLLPEQKAQALLLEVEEIFKNSPFLVPDGSVSIMDGSYEGILAWVT 178

Qy        204 INFLTGSLKTPGGSSVGMLDLGGGSTQIAFLPRVEGTLQASPPGYLTALRMFNRTYKLYS 263
              :||||| |   |  :|| ||||| |||| |||: | ||: :| ||||:  ||| |:|||:
Db        179 VNFLTGQLHGRGQETVGTLDLGGASTQITFLPQFEKTLEQTPRGYLTSFEMFNSTFKLYT 238

Qy        264 YSYLGLGLMSARLAILGGVEGQPAKDGKELVSPCLSPSFKGEWEHAEVTYRVSGQKAAAS 323
              :|||| || :|||| || :| :   ||    | ||    : ||    | |: | :
Db        239 HSYLGFGLKAARLATLGALEAK-GTDGHTFRSACLPRWLEAEWIFGGVKYQYGGNQEGEM 297

Qy        324 LHELCAARVSEVLQNRVHRTEEVKHVDFYAFSYYYDLAAGVGLIDAEKGGSLVVGDFEIA 383
                | | |  |:| ::|: |||:   |||||||| ||   ||| |||| | | |||

Db        298 GFEPCYAEVLRVVQGKLHQPEEVRGSAFYAFSYYYDRAADTHLIDYEKGGGVLKVEDFERK 357

Qy        384 AKYVCRTLETQPQSSPFSCMDLTYVSLLLQE-FGFPRSKVLKLTRKIDNVETSWALGAIF 442
              |: ||  | :    ||| |||||:: ||:: |||    :|:||:|::|:|| ||||| |
Db        358 AREVCDNLGSFSSGSPFLCMDLTYITALLKDGFGFADGTLLQLTKKVNNIETGWALGATF 417

Qy        443 HYIDSL 448
                | : ||
Db        418 HLLQSL 423


RESULT 10
Q8CD29
ID   Q8CD29      PRELIMINARY;      PRT;   427 AA.
AC   Q8CD29;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Mus musculus 13 days embryo male testis cDNA, RIKEN full-length
DE   enriched library, clone:6030456F04 product:ectonucleoside triphosphate
DE   diphosphohydrolase 5, full insert sequence.
GN   Name=Entpd5;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Testis;
RX   MEDLINE=99279253; PubMed=10349636;
RA   Carninci P., Hayashizaki Y.;
RT   "High-efficiency full-length cDNA cloning.";
RL   Meth. Enzymol. 303:19-44(1999).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Testis;
RX   MEDLINE=21085660; PubMed=11217851;
RA   RIKEN FANTOM Consortium;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Testis;
RA   The FANTOM Consortium,
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Testis;
RX   MEDLINE=20499374; PubMed=11042159;
RA   Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA   Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT   "Normalization and subtraction of cap-trapper-selected cDNAs to
RT   prepare full-length cDNA libraries for rapid discovery of new genes.";
RL   Genome Res. 10:1617-1630(2000).
RN   [5]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Testis;
RX   MEDLINE=20530913; PubMed=11076861;
RA   Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA   Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA   Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA   Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA   Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA   Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA   Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT   "RIKEN integrated sequence analysis (RISA) system-384-format
RT   sequencing pipeline with 384 multicapillary sequencer.";
RL   Genome Res. 10:1757-1771(2000).
RN   [6]
RP   SEQUENCE FROM N.A.
```

```
RC   STRAIN=C57BL/6J; TISSUE=Testis;
RA   Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA   Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA   Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA   Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA   Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA   Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA   Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA   Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA   Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA   Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA   Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AK031581; BAC27461.1; -.
DR   MGD; MGI:1321385; Entpd5.
DR   GO; GO:0016787; F:hydrolase activity; IEA.
DR   InterPro; IPR000407; GDA1_CD39_NTPase.
DR   Pfam; PF01150; GDA1_CD39; 1.
KW   Hydrolase.
SQ   SEQUENCE   427 AA;  47101 MW;  6E3773C842B58477 CRC64;

  Query Match             42.6%;  Score 1007;  DB 2;  Length 427;
  Best Local Similarity   50.0%;  Pred. No. 8.8e-71;
  Matches  213;  Conservative   62;  Mismatches  133;  Indels   18;  Gaps    6;

Qy         37 ATATQAFFSITRAAPGA--------RWGQ----QAHSPLGTAADGHEVFYGIMFDAGSTG 84
              ||:  | | :  |  |:         | :     :  |:  :|     ||||||||||||
Db          2 ATSWGAVFMLIIACVGSTVFYREQQTWFEGVFLSSMCPINVSAG---TFYGIMFDAGSTG 58

Qy         85 TRVHVFQFT-RPPRETPTLTHETFKAVKPGLSAYADDVEKSAQGIRELLDVAKQDIPFDF 143
              ||:||:  |  :   : | |  | | :|||||||: |  :: |: ::|||:|||  ||
Db         59 TRIHVYTFVQKTAGQLPFLEGEIFDSVKPGLSAFVDQPKQGAETVQELLEVAKDSIPRSH 118

Qy        144 WKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASPFLVGDDCVSIMNGTDEGVSAWIT 203
              |: ||:|||||||||||| :||| || :|:|:|| ||||| |  ||||:|: ||: ||:|
Db        119 WERTPVVLKATAGLRLLPEQKAQALLLEVEEIFKNSPFLVPDGSVSIMDGSYEGILAWVT 178

Qy        204 INFLTGSLKTPGGSSVGMLDLGGGSTQIAFLPRVEGTLQASPPGYLTALRMFNRTYKLYS 263
              :||||| |   |  :|| ||||| |||| |||: | ||: :| ||||:  ||| |:|||:
Db        179 VNFLTGQLHGRGQETVGTLDLGGASTQITFLPQFEKTLEKTPRGYLTSFEMFNSTFKLYT 238

Qy        264 YSYLGLGLMSARLAILGGVEGQPAKDGKELVSPCLSPSFKGEWEHAEVTYRVSGQKAAAS 323
              :|||| || :|||| || :| :   ||    | ||    : ||    | |:  | :
Db        239 HSYLGFGLKAARLATLGALEAK-GTDGHTFRSACLPRWLEAEWIFGGVKYQYGGNQEGEM 297

Qy        324 LHELCAARVSEVLQNRVHRTEEVKHVDFYAFSYYYDLAAGVGLIDAEKGGSLVVGDFEIA 383
              | | | |  |:| ::|: |||:   |||||||||| ||   ||| |||| | | |||
Db        298 GFEPCYAEVLRVVQGKLHQPEEVRGSAFYAFSYYYDRAADTHLIDYEKGGVLKVEDFERK 357

Qy        384 AKYVCRTLETQPQSSPFSCMDLTYVSLLLQE-FGFPRSKVLKLTRKIDNVETSWALGAIF 442
              |: ||  | :    ||| ||||||:: ||:: |||    :|:||:|::|:|| ||||| |
Db        358 AREVCDNLGSFSSGSPFLCMDLTYITALLKDGFGFADGTLLQLTKKVNNIETGWALGATF 417

Qy        443 HYIDSL 448
              | : ||
Db        418 HLLQSL 423


RESULT 11
AAK82949
ID   AAK82949    PRELIMINARY;      PRT;   427 AA.
AC   AAK82949;
DT   02-MAR-2004 (TrEMBLrel. 27, Created)
DT   02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT   02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE   Pcph proto-oncogene protein.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=thymus;
RX   MEDLINE=99437879; PubMed=10506756;
RA   Recio J.A., Zambrano N., de La Pena L., Powers C., Siwarski D.,
RA   Huppi K., Notario V.;
RT   "cDNA isolation, expression, and chromosomal localization of the mouse
RT   pcph proto-oncogene.";
RL   Mol. Carcinog. 26:130-136(1999).
DR   EMBL; AF136571; AAK82949.1; -.
SQ   SEQUENCE   427 AA;  47101 MW;  2F9DA2C342C55577 CRC64;

  Query Match             42.6%;  Score 1007;  DB 2;  Length 427;
  Best Local Similarity   50.0%;  Pred. No. 8.8e-71;
  Matches  213;  Conservative   62;  Mismatches  133;  Indels   18;  Gaps    6;

Qy         37 ATATQAFFSITRAAPGA--------RWGQ----QAHSPLGTAADGHEVFYGIMFDAGSTG 84
              ||:  | | :  |  |:         | :     :  |:  :|     ||||||||||||
Db          2 ATSWGAVFMLIIACVGSTVFYREQQTWFEGVFLSSMCPINVSAG---TFYGIMFDAGSTG 58

Qy         85 TRVHVFQFT-RPPRETPTLTHETFKAVKPGLSAYADDVEKSAQGIRELLDVAKQDIPFDF 143
              ||:||:  |  :   : | |  | | :|||||||: |  :: |: ::|||:|||  ||
Db         59 TRIHVYTFVQKTAGQLPFLEGEIFDSVKPGLSAFVDQPKQGAETVQELLEVAKDSIPRSH 118

Qy        144 WKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASPFLVGDDCVSIMNGTDEGVSAWIT 203
              |: ||:|||||||||||| :||| || :|:|:|| ||||| |  ||||:|: ||: ||:|
Db        119 WERTPVVLKATAGLRLLPEQKAQALLLEVEEIFKNSPFLVPDGSVSIMDGSYEGILAWVT 178

Qy        204 INFLTGSLKTPGGSSVGMLDLGGGSTQIAFLPRVEGTLQASPPGYLTALRMFNRTYKLYS 263
              :||||| |   |  :|| ||||| |||| |||: | ||: :| ||||:  ||| |:|||:
Db        179 VNFLTGQLHGRGQETVGTLDLGGASTQITFLPQFEKTLEQTPRGYLTSFEMFNSTFKLYT 238

Qy        264 YSYLGLGLMSARLAILGGVEGQPAKDGKELVSPCLSPSFKGEWEHAEVTYRVSGQKAAAS 323
              :|||| || :|||| || :| :   ||    | ||    : ||    | |:  | :
Db        239 HSYLGFGLKAARLATLGALEAK-GTDGHTFRSACLPRWLEAEWIFGGVKYQYGGNQEGEM 297

Qy        324 LHELCAARVSEVLQNRVHRTEEVKHVDFYAFSYYYDLAAGVGLIDAEKGGSLVVGDFEIA 383
              | | | |  |:| ::|: |||:   |||||||||| ||   ||| |||| | | |||
Db        298 GFEPCYAEVLRVVQGKLHQPEEVRGSAFYAFSYYYDRAADTHLIDYEKGGVLKVEDFERK 357

Qy        384 AKYVCRTLETQPQSSPFSCMDLTYVSLLLQE-FGFPRSKVLKLTRKIDNVETSWALGAIF 442
              |: ||  | :    ||| ||||||:: ||:: |||    :|:||:|::|:|| ||||| |
Db        358 AREVCDNLGSFSSGSPFLCMDLTYITALLKDGFGFADGTLLQLTKKVNNIETGWALGATF 417

Qy        443 HYIDSL 448
              | : ||
Db        418 HLLQSL 423


RESULT 12
BAC29515
ID   BAC29515    PRELIMINARY;      PRT;   427 AA.
AC   BAC29515;
DT   14-APR-2004 (TrEMBLrel. 27, Created)
DT   14-APR-2004 (TrEMBLrel. 27, Last sequence update)
DT   14-APR-2004 (TrEMBLrel. 27, Last annotation update)
DE   Adult male bone cDNA, RIKEN full-length enriched library,
DE   clone:9830144N04 product:ectonucleoside triphosphate
DE   diphosphohydrolase 5, full insert sequence.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Bone;
RX   MEDLINE=22354683; PubMed=12466851;
RA   The FANTOM Consortium,
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Bone;
RX   MEDLINE=21085660; PubMed=11217851;
```

```
RA   RIKEN FANTOM Consortium;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Bone;
RX   MEDLINE=99279253; PubMed=10349636;
RA   Carninci P., Hayashizaki Y.;
RT   "High-efficiency full-length cDNA cloning.";
RL   Meth. Enzymol. 303:19-44(1999).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Bone;
RX   MEDLINE=20499374; PubMed=11042159;
RA   Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA   Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT   "Normalization and subtraction of cap-trapper-selected cDNAs to
RT   prepare full-length cDNA libraries for rapid discovery of new genes.";
RL   Genome Res. 10:1617-1630(2000).
RN   [5]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Bone;
RX   MEDLINE=20530913; PubMed=11076861;
RA   Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA   Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA   Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA   Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA   Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA   Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA   Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT   "RIKEN integrated sequence analysis (RISA) system-384-format
RT   sequencing pipeline with 384 multicapillary sequencer.";
RL   Genome Res. 10:1757-1771(2000).
RN   [6]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Bone;
RA   Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA   Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA   Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA   Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA   Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA   Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA   Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA   Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA   Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA   Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA   Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AK036641; BAC29515.1; -.
KW   Hydrolase.
SQ   SEQUENCE   427 AA;  47101 MW;  2F9DA2C342C55577 CRC64;

  Query Match           42.6%;  Score 1007;  DB 2;  Length 427;
  Best Local Similarity  50.0%;  Pred. No. 8.8e-71;
  Matches  213;  Conservative   62;  Mismatches  133;  Indels   18;  Gaps    6;

Qy         37 ATATQAFFSITRAAPGA--------RWGQ----QAHSPLGTAADGHEVFYGIMFDAGSTG 84
              ||:  | | :  |  |:         | :     :  |:  :|     ||||||||||||
Db          2 ATSWGAVFMLIIACVGSTVFYREQQTWFEGVFLSSMCPINVSAG---TFYGIMFDAGSTG 58

Qy         85 TRVHVFQFT-RPPRETPTLTHETFKAVKPGLSAYADDVEKSAQGIRELLDVAKQDIPFDF 143
              ||:||: |  :   : | |  | | :|||||||: |  :: |: ::|||:|||  ||
Db         59 TRIHVYTFVQKTAGQLPFLEGEIFDSVKPGLSAFVDQPKQGAETVQELLEVAKDSIPRSH 118

Qy        144 WKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASPFLVGDDCVSIMNGTDEGVSAWIT 203
              |: ||:|||||||||||| :||| || :|:|:|| ||||| |  ||||:|: ||: ||:|
Db        119 WERTPVVLKATAGLRLLPEQKAQALLLEVEEIFKNSPFLVPDGSVSIMDGSYEGILAWVT 178

Qy        204 INFLTGSLKTPGGSSVGMLDLGGGSTQIAFLPRVEGTLQASPPGYLTALRMFNRTYKLYS 263
              :|||||  |   :|| ||||| |||| |||: | ||: :| ||||:  ||| |:|||:
Db        179 VNFLTGQLHGRGQETVGTLDLGGASTQITFLPQFEKTLEQTPRGYLTSFEMFNSTFKLYT 238

Qy        264 YSYLGLGLMSARLAILGGVEGQPAKDGKELVSPCLSPSFKGEWEHAEVTYRVSGQKAAAS 323
              :|||| || :|||| || :| :   ||    | ||    : ||    | |:  | :
Db        239 HSYLGFGLKAARLATLGALEAK-GTDGHTFRSACLPRWLEAEWIFGGVKYQYGGNQEGEM 297

Qy        324 LHELCAARVSEVLQNRVHRTEEVKHVDFYAFSYYYDLAAGVGLIDAEKGGSLVVGDFEIA 383
              | | | |  |:| ::|: |||:   |||||||||| ||   ||| |||| | | |||
Db        298 GFEPCYAEVLRVVQGKLHQPEEVRGSAFYAFSYYYDRAADTHLIDYEKGGVLKVEDFERK 357

Qy        384 AKYVCRTLETQPQSSPFSCMDLTYVSLLLQE-FGFPRSKVLKLTRKIDNVETSWALGAIF 442
              |: ||  | :    ||| |||||:: ||:: |||    :|:||:|::|:|| ||||| |
Db        358 AREVCDNLGSFSSGSPFLCMDLTYITALLKDGFGFADGTLLQLTKKVNNIETGWALGATF 417

Qy        443 HYIDSL 448
              | : ||
Db        418 HLLQSL 423


RESULT 13
BAC29861
ID   BAC29861    PRELIMINARY;      PRT;   427 AA.
AC   BAC29861;
DT   14-APR-2004 (TrEMBLrel. 27, Created)
DT   14-APR-2004 (TrEMBLrel. 27, Last sequence update)
DT   14-APR-2004 (TrEMBLrel. 27, Last annotation update)
DE   16 days neonate thymus cDNA, RIKEN full-length enriched library,
DE   clone:A130044A06 product:ectonucleoside triphosphate
DE   diphosphohydrolase 5, full insert sequence.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Thymus;
RX   MEDLINE=22354683; PubMed=12466851;
RA   The FANTOM Consortium,
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Thymus;
RX   MEDLINE=21085660; PubMed=11217851;
RA   RIKEN FANTOM Consortium;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Thymus;
RX   MEDLINE=99279253; PubMed=10349636;
RA   Carninci P., Hayashizaki Y.;
RT   "High-efficiency full-length cDNA cloning.";
RL   Meth. Enzymol. 303:19-44(1999).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Thymus;
RX   MEDLINE=20499374; PubMed=11042159;
RA   Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA   Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT   "Normalization and subtraction of cap-trapper-selected cDNAs to
RT   prepare full-length cDNA libraries for rapid discovery of new genes.";
RL   Genome Res. 10:1617-1630(2000).
RN   [5]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Thymus;
RX   MEDLINE=20530913; PubMed=11076861;
RA   Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA   Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA   Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA   Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA   Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA   Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA   Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
```

```
RT   "RIKEN integrated sequence analysis (RISA) system-384-format
RT   sequencing pipeline with 384 multicapillary sequencer.";
RL   Genome Res. 10:1757-1771(2000).
RN   [6]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Thymus;
RA   Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA   Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA   Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA   Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA   Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA   Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA   Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA   Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA   Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA   Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA   Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AK037736; BAC29861.1; -.
KW   Hydrolase.
SQ   SEQUENCE   427 AA;  47101 MW;  2F9DA2C342C55577 CRC64;

  Query Match             42.6%;  Score 1007;  DB 2;  Length 427;
  Best Local Similarity   50.0%;  Pred. No. 8.8e-71;
  Matches  213;  Conservative   62;  Mismatches  133;  Indels   18;  Gaps    6;

Qy         37 ATATQAFFSITRAAPGA--------RWGQ----QAHSPLGTAADGHEVFYGIMFDAGSTG 84
              ||:  | | :  |  |:          | :     :  |:  :|     ||||||||||||
Db          2 ATSWGAVFMLIIACVGSTVFYREQQTWFEGVFLSSMCPINVSAG---TFYGIMFDAGSTG 58

Qy         85 TRVHVFQFT-RPPRETPTLTHETFKAVKPGLSAYADDVEKSAQGIRELLDVAKQDIPFDF 143
              ||:||: |  :   : | |  | | :|||||||: |  :: |: ::|||:|||  ||
Db         59 TRIHVYTFVQKTAGQLPFLEGEIFDSVKPGLSAFVDQPKQGAETVQELLEVAKDSIPRSH 118

Qy        144 WKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASPFLVGDDCVSIMNGTDEGVSAWIT 203
              |: ||:|||||||||||| :||| || :|:|:|| ||||| |  ||||:|: ||: ||:|
Db        119 WERTPVVLKATAGLRLLPEQKAQALLLEVEEIFKNSPFLVPDGSVSIMDGSYEGILAWVT 178

Qy        204 INFLTGSLKTPGGSSVGMLDLGGGSTQIAFLPRVEGTLQASPPGYLTALRMFNRTYKLYS 263
              :||||| |   |  :|| ||||| |||| |||: | ||: :| ||||:  ||| |:|||:
Db        179 VNFLTGQLHGRGQETVGTLDLGGASTQITFLPQFEKTLEQTPRGYLTSFEMFNSTFKLYT 238

Qy        264 YSYLGLGLMSARLAILGGVEGQPAKDGKELVSPCLSPSFKGEWEHAEVTYRVSGQKAAAS 323
              :|||| || :|||| || :| :   ||    | ||    : ||    | |:  | :
Db        239 HSYLGFGLKAARLATLGALEAK-GTDGHTFRSACLPRWLEAEWIFGGVKYQYGGNQEGEM 297

Qy        324 LHELCAARVSEVLQNRVHRTEEVKHVDFYAFSYYYDLAAGVGLIDAEKGGSLVVGDFEIA 383
              | | | |  |:| ::|: |||:   |||||||| ||   ||| |||| | | |||
Db        298 GFEPCYAEVLRVVQGKLHQPEEVRGSAFYAFSYYYDRAADTHLIDYEKGGVLKVEDFERK 357

Qy        384 AKYVCRTLETQPQSSPFSCMDLTYVSLLLQE-FGFPRSKVLKLTRKIDNVETSWALGAIF 442
              |: ||  | :    ||| |||||:: ||:: |||    :|:||:|::|:|| |||||
Db        358 AREVCDNLGSFSSGSPFLCMDLTYITALLKDGFGFADGTLLQLTKKVNNIETGWALGATF 417

Qy        443 HYIDSL 448
              | : ||
Db        418 HLLQSL 423


RESULT 14
BAC37592
ID   BAC37592    PRELIMINARY;      PRT;   427 AA.
AC   BAC37592;
DT   14-APR-2004 (TrEMBLrel. 27, Created)
DT   14-APR-2004 (TrEMBLrel. 27, Last sequence update)
DT   14-APR-2004 (TrEMBLrel. 27, Last annotation update)
DE   Adult male urinary bladder cDNA, RIKEN full-length enriched library,
DE   clone:9530068A17 product:ectonucleoside triphosphate
DE   diphosphohydrolase 5, full insert sequence.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Urinary bladder;
RX   MEDLINE=22354683; PubMed=12466851;
RA   The FANTOM Consortium,
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Urinary bladder;
RX   MEDLINE=21085660; PubMed=11217851;
RA   RIKEN FANTOM Consortium;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Urinary bladder;
RX   MEDLINE=99279253; PubMed=10349636;
RA   Carninci P., Hayashizaki Y.;
RT   "High-efficiency full-length cDNA cloning.";
RL   Meth. Enzymol. 303:19-44(1999).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Urinary bladder;
RX   MEDLINE=20499374; PubMed=11042159;
RA   Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA   Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT   "Normalization and subtraction of cap-trapper-selected cDNAs to
RT   prepare full-length cDNA libraries for rapid discovery of new genes.";
RL   Genome Res. 10:1617-1630(2000).
RN   [5]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Urinary bladder;
RX   MEDLINE=20530913; PubMed=11076861;
RA   Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA   Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA   Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA   Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA   Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA   Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA   Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT   "RIKEN integrated sequence analysis (RISA) system-384-format
RT   sequencing pipeline with 384 multicapillary sequencer.";
RL   Genome Res. 10:1757-1771(2000).
RN   [6]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Urinary bladder;
RA   Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA   Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA   Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA   Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA   Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA   Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA   Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA   Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA   Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA   Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA   Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL   Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AK079267; BAC37592.1; -.
KW   Hydrolase.
SQ   SEQUENCE   427 AA;  47101 MW;  2F9DA2C342C55577 CRC64;

  Query Match             42.6%;  Score 1007;  DB 2;  Length 427;
  Best Local Similarity   50.0%;  Pred. No. 8.8e-71;
  Matches  213;  Conservative   62;  Mismatches  133;  Indels   18;  Gaps    6;

Qy         37 ATATQAFFSITRAAPGA--------RWGQ----QAHSPLGTAADGHEVFYGIMFDAGSTG 84
              ||:  | | :  |  |:          | :     :  |:  :|     ||||||||||||
Db          2 ATSWGAVFMLIIACVGSTVFYREQQTWFEGVFLSSMCPINVSAG---TFYGIMFDAGSTG 58
```

```
Qy          85 TRVHVFQFT-RPPRETPTLTHETFKAVKPGLSAYADDVEKSAQGIRELLDVAKQDIPFDF 143
               ||:||: |  :   : | |  | | :|||||||: |  :: |: ::|||:|||  ||
Db          59 TRIHVYTFVQKTAGQLPFLEGEIFDSVKPGLSAFVDQPKQGAETVQELLEVAKDSIPRSH 118

Qy         144 WKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASPFLVGDDCVSIMNGTDEGVSAWIT 203
               |: ||:|||||||||||| :||| || :|:|:|| ||||| |  ||||:|: ||: ||:|
Db         119 WERTPVVLKATAGLRLLPEQKAQALLLEVEEIFKNSPFLVPDGSVSIMDGSYEGILAWVT 178

Qy         204 INFLTGSLKTPGGSSVGMLDLGGGSTQIAFLPRVEGTLQASPPGYLTALRMFNRTYKLYS 263
               :||||| |   |  :|| |||| |||| ||: | ||: :| ||||:  ||| |:|||:
Db         179 VNFLTGQLHGRGQETVGTLDLGGASTQITFLPQFEKTLEQTPRGYLTSFEMFNSTFKLYT 238

Qy         264 YSYLGLGLMSARLAILGGVEGQPAKDGKELVSPCLSPSFKGEWEHAEVTYRVSGQKAAAS 323
               :|||| || :|||| || :| :   ||    | ||    : ||    | |:  | :
Db         239 HSYLGFGLKAARLATLGALEAK-GTDGHTFRSACLPRWLEAEWIFGGVKYQYGGNQEGEM 297

Qy         324 LHELCAARVSEVLQNRVHRTEEVKHVDFYAFSYYYDLAAGVGLIDAEKGGSLVVGDFEIA 383
               | | | |  |:| ::|: |||:   |||||||| ||   ||| |||| | | |||
Db         298 GFEPCYAEVLRVVQGKLHQPEEVRGSAFYAFSYYYDRAADTHLIDYEKGGVLKVEDFERK 357

Qy         384 AKYVCRTLETQPQSSPFSCMDLTYVSLLLQE-FGFPRSKVLKLTRKIDNVETSWALGAIF 442
               |: ||  | :   ||| ||||||:: ||:: |||    :|:||:|::|:|| ||||| |
Db         358 AREVCDNLGSFSSGSPFLCMDLTYITALLKDGFGFADGTLLQLTKKVNNIETGWALGATF 417

Qy         443 HYIDSL 448
               | : ||
Db         418 HLLQSL 423
```

```
RESULT 15
BAC37862
ID   BAC37862    PRELIMINARY;      PRT;   427 AA.
AC   BAC37862;
DT   14-APR-2004 (TrEMBLrel. 27, Created)
DT   14-APR-2004 (TrEMBLrel. 27, Last sequence update)
DT   14-APR-2004 (TrEMBLrel. 27, Last annotation update)
DE   3 days neonate thymus cDNA, RIKEN full-length enriched library,
DE   clone:A630007L13 product:ectonucleoside triphosphate
DE   diphosphohydrolase 5, full insert sequence.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Thymus;
RX   MEDLINE=22354683; PubMed=12466851;
RA   The FANTOM Consortium,
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Thymus;
RX   MEDLINE=21085660; PubMed=11217851;
RA   RIKEN FANTOM Consortium;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Thymus;
RX   MEDLINE=99279253; PubMed=10349636;
RA   Carninci P., Hayashizaki Y.;
RT   "High-efficiency full-length cDNA cloning.";
RL   Meth. Enzymol. 303:19-44(1999).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Thymus;
RX   MEDLINE=20499374; PubMed=11042159;
RA   Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA   Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT   "Normalization and subtraction of cap-trapper-selected cDNAs to
RT   prepare full-length cDNA libraries for rapid discovery of new genes.";
RL   Genome Res. 10:1617-1630(2000).
RN   [5]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Thymus;
RX   MEDLINE=20530913; PubMed=11076861;
RA   Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA   Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA   Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA   Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA   Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA   Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA   Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT   "RIKEN integrated sequence analysis (RISA) system-384-format
RT   sequencing pipeline with 384 multicapillary sequencer.";
RL   Genome Res. 10:1757-1771(2000).
RN   [6]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Thymus;
RA   Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA   Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA   Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA   Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA   Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA   Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA   Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA   Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA   Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA   Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA   Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL   Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AK080265; BAC37862.1; -.
KW   Hydrolase.
SQ   SEQUENCE   427 AA;  47101 MW;  2F9DA2C342C55577 CRC64;

  Query Match             42.6%;  Score 1007;  DB 2;  Length 427;
  Best Local Similarity   50.0%;  Pred. No. 8.8e-71;
  Matches  213;  Conservative   62;  Mismatches  133;  Indels   18;  Gaps    6;

Qy          37 ATATQAFFSITRAAPGA--------RWGQ----QAHSPLGTAADGHEVFYGIMFDAGSTG 84
               ||:  | | :  |  |:          | :     :  |:  :|     ||||||||||||
Db           2 ATSWGAVFMLIIACVGSTVFYREQQTWFEGVFLSSMCPINVSAG---TFYGIMFDAGSTG 58

Qy          85 TRVHVFQFT-RPPRETPTLTHETFKAVKPGLSAYADDVEKSAQGIRELLDVAKQDIPFDF 143
               ||:||: |  :   : | |  | | :|||||||: |  :: |: ::|||:|||  ||
Db          59 TRIHVYTFVQKTAGQLPFLEGEIFDSVKPGLSAFVDQPKQGAETVQELLEVAKDSIPRSH 118

Qy         144 WKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASPFLVGDDCVSIMNGTDEGVSAWIT 203
               |: ||:|||||||||||| :||| || :|:|:|| ||||| |  ||||:|: ||: ||:|
Db         119 WERTPVVLKATAGLRLLPEQKAQALLLEVEEIFKNSPFLVPDGSVSIMDGSYEGILAWVT 178

Qy         204 INFLTGSLKTPGGSSVGMLDLGGGSTQIAFLPRVEGTLQASPPGYLTALRMFNRTYKLYS 263
               :||||| |   |  :|| |||| |||| ||: | ||: :| ||||:  ||| |:|||:
Db         179 VNFLTGQLHGRGQETVGTLDLGGASTQITFLPQFEKTLEQTPRGYLTSFEMFNSTFKLYT 238

Qy         264 YSYLGLGLMSARLAILGGVEGQPAKDGKELVSPCLSPSFKGEWEHAEVTYRVSGQKAAAS 323
               :|||| || :|||| || :| :   ||    | ||    : ||    | |:  | :
Db         239 HSYLGFGLKAARLATLGALEAK-GTDGHTFRSACLPRWLEAEWIFGGVKYQYGGNQEGEM 297

Qy         324 LHELCAARVSEVLQNRVHRTEEVKHVDFYAFSYYYDLAAGVGLIDAEKGGSLVVGDFEIA 383
               | | | |  |:| ::|: |||:   |||||||| ||   ||| |||| | | |||
Db         298 GFEPCYAEVLRVVQGKLHQPEEVRGSAFYAFSYYYDRAADTHLIDYEKGGVLKVEDFERK 357

Qy         384 AKYVCRTLETQPQSSPFSCMDLTYVSLLLQE-FGFPRSKVLKLTRKIDNVETSWALGAIF 442
               |: ||  | :   ||| ||||||:: ||:: |||    :|:||:|::|:|| ||||| |
Db         358 AREVCDNLGSFSSGSPFLCMDLTYITALLKDGFGFADGTLLQLTKKVNNIETGWALGATF 417

Qy         443 HYIDSL 448
               | : ||
Db         418 HLLQSL 423


Search completed: November 16, 2004, 16:59:41
```

Job time : 201 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: November 16, 2004, 16:32:53 ; Search time 156 Seconds
(without alignments)
1048.593 Million cell updates/sec

Title: US-09-905-589A-2
Perfect score: 2364
Sequence: 1 MRKISNHGSLRVAKVAYPLG.....ALGAIFHYIDSLNRQKSPAS 456

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2364	100.0	456	5	AAE19881	Aae19881 Human CD3
2	2364	100.0	456	8	ADQ99442	Adq99442 Human CD3
3	2364	100.0	484	4	AAB72241	Aab72241 Human CD3
4	2364	100.0	484	8	ADQ99473	Adq99473 Human CD3
5	2361	99.9	463	5	ABB06124	Abb06124 Human NS
6	2361	99.9	467	5	ABJ04657	Abj04657 Protein o
7	2351	99.5	456	4	AAM93929	Aam93929 Human pol
8	2351	99.5	456	8	ADL32067	Adl32067 Human pro
9	2152	91.0	450	7	ADC14220	Adc14220 Human enz
10	2135	90.3	462	4	AAU30882	Aau30882 Novel hum
11	2116	89.5	446	5	ABJ04658	Abj04658 Protein o
12	2003	84.7	471	4	AAB72242	Aab72242 Mature hu
13	999	42.3	428	3	AAY44849	Aay44849 Human CD3
14	999	42.3	428	4	AAB72238	Aab72238 Human CD3
15	999	42.3	428	4	AAB72243	Aab72243 Human CD3
16	999	42.3	428	5	AAE19883	Aae19883 Human CD3
17	999	42.3	428	8	ADP07487	Adp07487 Human CD3
18	999	42.3	428	8	ADP07485	Adp07485 Human CD3
19	999	42.3	428	8	ADQ99446	Adq99446 Human CD3
20	999	42.3	428	8	ADQ99449	Adq99449 Human CD3
21	996	42.1	428	3	AAY44850	Aay44850 Human CD3
22	996	42.1	428	4	AAB72240	Aab72240 Human CD3
23	992	42.0	428	7	ADJ70490	Adj70490 Human hea
24	992	42.0	428	8	ADP07489	Adp07489 Human CD3
25	909	38.5	405	3	AAY44851	Aay44851 Human CD3
26	909	38.5	405	4	AAB72239	Aab72239 Human CD3
27	909	38.5	407	8	ADP07491	Adp07491 Human CD3
28	904	38.2	465	5	AAE19884	Aae19884 Mouse CD3
29	904	38.2	465	8	ADQ99448	Adq99448 Mouse CD3
30	823	34.8	330	3	AAB53336	Aab53336 Human col
31	621	26.3	461	4	ABB66213	Abb66213 Drosophil
32	621	26.3	461	8	ADQ99472	Adq99472 Human NTP
33	621	26.3	464	4	ABB59611	Abb59611 Drosophil
34	596	25.2	141	4	AAU30879	Aau30879 Novel hum
35	596	25.2	144	4	AAU30881	Aau30881 Novel hum
36	518.5	21.9	467	2	AAW85687	Aaw85687 DBX oligo
37	506	21.4	462	2	AAW85684	Aaw85684 NBP46 roo
38	506	21.4	462	5	AAU78818	Aau78818 Dolichos
39	501	21.2	486	2	AAW85685	Aaw85685 NBP46 roo
40	501	21.2	486	5	AAU78819	Aau78819 Lotus jap
41	495	20.9	139	5	ADK36500	Adk36500 Novel hum
42	490	20.7	455	8	ADO60417	Ado60417 Toxic sub
43	488.5	20.7	472	6	ABP81286	Abp81286 Arabidops
44	486	20.6	457	7	ABM74049	Abm74049 DNA clone
45	485	20.5	454	7	ADJ57264	Adj57264 Potato ap

ALIGNMENTS

RESULT 1
AAE19881
ID AAE19881 standard; protein; 456 AA.
XX
AC AAE19881;
XX
DT 18-JUN-2002 (first entry)
XX
DE Human CD39L2 protein.
XX
KW Human; CD-39-like protein; CD39L2 protein; therapy; immune deficiency;
KW autoimmune disorder; multiple sclerosis; systemic lupus erythematosus;
KW rheumatoid arthritis; autoimmune thyroiditis; allergic reaction; asthma;
KW insulin dependent diabetes mellitus; periodontal disease; osteoporosis;
KW osteoarthritis; wound healing; tissue repair; Alzheimer's disease; ulcer;
KW Parkinson's disease; amyotrophic lateral sclerosis; Huntington's disease;
KW nervous system disease; nerve injury; ischaemia-reperfusion injury;
KW endotoxin lethality; arthritis; nephritis; inflammatory bowel disease;
KW Crohn's disease; virucide; antibacterial; antifungal; neuroprotective;
KW dermatological; immunosuppressive; vulnerary; nootropic; anticonvulsant;
KW antiinflammatory; nephrotropic; gastrointestinal; vasotropic.
XX
OS Homo sapiens.
XX
PN US6350447-B1.
XX
PD 26-FEB-2002.
XX
PF 29-JAN-1999; 99US-00240639.
XX
PR 29-JAN-1999; 99US-00240639.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Chadwick BP, Frischauf A;
XX
DR WPI; 2002-215262/27.
DR N-PSDB; AAD31693.
XX
PT An isolated polypeptide with phosphohydrolase activity, designated
PT CD39L2, useful to identify other proteins with which binding occurs or
PT identify inhibitors and for treatment of, e.g., Alzheimer's, multiple
PT sclerosis and osteoporosis.
XX
PS Claim 1; Fig 4; 101pp; English.
XX
CC The present invention relates to novel proteins with phosphohydrolase
CC activity, designated CD-39-like (CD39L) proteins and polynucleotides

```
CC   encoding such proteins. CD39L proteins are useful to treat infectious
CC   diseases caused by viral, bacterial, fungal or other infection that may
CC   be treatable with CD39L. They are useful in the treatment of various
CC   immune deficiencies and disorders, autoimmune disorders such as multiple
CC   sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune
CC   thyroiditis and insulin dependent diabetes mellitus, allergic reactions
CC   and conditions such as asthma and other respiratory problems, periodontal
CC   disease, osteoporosis, osteoarthritis and other tooth repair processes.
CC   They may have utility in compositions used for bone, cartilage, tendon,
CC   ligament and/or nerve tissue growth or regeneration as well as for wound
CC   healing and tissue repair and replacement and in the treatment of burns,
CC   incisions and ulcers. CD39L proteins may also be useful for proliferation
CC   of neural cells and for regeneration of nerve and brain tissue, i.e. for
CC   the treatment of central nervous system diseases such as Alzheimer's
CC   disease, Parkinson's disease, amyotrophic lateral sclerosis, Huntington's
CC   disease, peripheral nervous system diseases peripheral nerve injuries,
CC   peripheral neuropathy and localised neuropathies. They are also used to
CC   treat mechanical and traumatic disorders which involve degeneration,
CC   death or trauma to neural cells or nerve tissue. CD39L proteins of the
CC   invention are also useful to promote better or faster closure of non-
CC   healing wounds, including pressure ulcers, ulcers associated with
CC   vascular insufficiency and surgical and traumatic wounds. They also
CC   exhibit anti-inflammatory activity and may be used to treat inflammatory
CC   conditions including chronic or acute conditions), including ischaemia-
CC   reperfusion injury, endotoxin lethality, arthritis, nephritis, cytokine
CC   or chemokine-induced lung injury, inflammatory bowel disease or Crohn's
CC   disease. The present sequence is human CD39L2 protein
XX
SQ   Sequence 456 AA;

  Query Match             100.0%;  Score 2364;  DB 5;  Length 456;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-215;
  Matches  456;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRKISNHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRATATQAFFSITRAAPGARWGQQAH 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRKISNHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRATATQAFFSITRAAPGARWGQQAH 60

Qy         61 SPLGTAADGHEVFYGIMFDAGSTGTRVHVFQFTRPPRETPTLTHETFKAVKPGLSAYADD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SPLGTAADGHEVFYGIMFDAGSTGTRVHVFQFTRPPRETPTLTHETFKAVKPGLSAYADD 120

Qy        121 VEKSAQGIRELLDVAKQDIPFDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASP 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VEKSAQGIRELLDVAKQDIPFDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASP 180

Qy        181 FLVGDDCVSIMNGTDEGVSAWITINFLTGSLKTPGGSSVGMLDLGGGSTQIAFLPRVEGT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 FLVGDDCVSIMNGTDEGVSAWITINFLTGSLKTPGGSSVGMLDLGGGSTQIAFLPRVEGT 240

Qy        241 LQASPPGYLTALRMFNRTYKLYSYSYLGLGLMSARLAILGGVEGQPAKDGKELVSPCLSP 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 LQASPPGYLTALRMFNRTYKLYSYSYLGLGLMSARLAILGGVEGQPAKDGKELVSPCLSP 300

Qy        301 SFKGEWEHAEVTYRVSGQKAAASLHELCAARVSEVLQNRVHRTEEVKHVDFYAFSYYYDL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 SFKGEWEHAEVTYRVSGQKAAASLHELCAARVSEVLQNRVHRTEEVKHVDFYAFSYYYDL 360

Qy        361 AAGVGLIDAEKGGSLVVGDFEIAAKYVCRTLETQPQSSPFSCMDLTYVSLLLQEFGFPRS 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAGVGLIDAEKGGSLVVGDFEIAAKYVCRTLETQPQSSPFSCMDLTYVSLLLQEFGFPRS 420

Qy        421 KVLKLTRKIDNVETSWALGAIFHYIDSLNRQKSPAS 456
              ||||||||||||||||||||||||||||||||||||
Db        421 KVLKLTRKIDNVETSWALGAIFHYIDSLNRQKSPAS 456


RESULT 2
ADQ99442
ID   ADQ99442 standard; protein; 456 AA.
XX
AC   ADQ99442;
XX
DT   23-SEP-2004  (first entry)
XX
DE   Human CD39-like protein, CD39L2.
XX
KW   CD39-like protein; gene mapping; molecular weight marker;
KW   food supplement; anti-thrombotic; anti-tissue graft rejection agent;
KW   ATP neurotransmission; ecto-ATPase activity; nucleotide triphosphatase;
KW   NTPase; human; enzyme.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Region          100. .121
FT                   /note= "Apyrase region (ACR) I"
FT   Region          175. .190
FT                   /note= "Apyrase region (ACR) II"
FT   Region          219. .239
FT                   /note= "Apyrase region (ACR) III"
FT   Region          245. .266
FT                   /note= "Apyrase region (ACR) IV"
XX
PN   US6759214-B1.
XX
PD   06-JUL-2004.
XX
PF   13-JUL-2001; 2001US-00908510.
XX
PR   29-JAN-1999;   99US-00240639.
XX
PA   (NUVE-) NUVELO INC.
XX
PI   Chadwick BP,  Frischauf A;
XX
DR   WPI; 2004-515395/49.
DR   N-PSDB; ADQ99441.
XX
PT   New CD-39-like polypeptides and polynucleotides, useful in chromosome and
PT   gene mapping, as molecular weight markers, as food supplements, or as
PT   anti-thrombotic or anti-tissue graft rejection agents.
XX
PS   Claim 2; SEQ ID NO 2; 104pp; English.
XX
CC   The invention relates to novel CD39-like polypeptides (CD39-like
CC   nucleotide triphosphatase; NTPase) and nucleic acid molecules encoding
CC   such polypeptides. CD39-like polynucleotides may be used as hybridisation
CC   probes, PCR primers and in chromosome and gene mapping. Polypeptides of
CC   the invention may be used as molecular weight markers, as food
CC   supplements, in generating an antibody that specifically binds the
CC   polypeptide, as anti-thrombotic or anti-tissue graft rejection agents, or
CC   for regulating ATP neurotransmission in smooth muscle, peripheral ganglia
CC   or brain. Sequences of the invention are useful in modulating ecto-ATPase
CC   activity and for identifying compounds that modulate ecto-ATPase
CC   activity. The present sequence is human CD39-like protein, CD39L2. Note:
CC   This sequence is stated to be the same as that shown in Figures 8 and 9,
CC   however the sequence is truncated at it's N-terminal. The longer sequence
CC   is represented in ADQ99473.
XX
SQ   Sequence 456 AA;

  Query Match             100.0%;  Score 2364;  DB 8;  Length 456;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-215;
  Matches  456;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRKISNHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRATATQAFFSITRAAPGARWGQQAH 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRKISNHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRATATQAFFSITRAAPGARWGQQAH 60

Qy         61 SPLGTAADGHEVFYGIMFDAGSTGTRVHVFQFTRPPRETPTLTHETFKAVKPGLSAYADD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SPLGTAADGHEVFYGIMFDAGSTGTRVHVFQFTRPPRETPTLTHETFKAVKPGLSAYADD 120

Qy        121 VEKSAQGIRELLDVAKQDIPFDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASP 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db        121 VEKSAQGIRELLDVAKQDIPFDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASP 180

Qy        181 FLVGDDCVSIMNGTDEGVSAWITINFLTGSLKTPGGSSVGMLDLGGGSTQIAFLPRVEGT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 FLVGDDCVSIMNGTDEGVSAWITINFLTGSLKTPGGSSVGMLDLGGGSTQIAFLPRVEGT 240

Qy        241 LQASPPGYLTALRMFNRTYKLYSYSYLGLGLMSARLAILGGVEGQPAKDGKELVSPCLSP 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 LQASPPGYLTALRMFNRTYKLYSYSYLGLGLMSARLAILGGVEGQPAKDGKELVSPCLSP 300

Qy        301 SFKGEWEHAEVTYRVSGQKAAASLHELCAARVSEVLQNRVHRTEEVKHVDFYAFSYYYDL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 SFKGEWEHAEVTYRVSGQKAAASLHELCAARVSEVLQNRVHRTEEVKHVDFYAFSYYYDL 360

Qy        361 AAGVGLIDAEKGGSLVVGDFEIAAKYVCRTLETQPQSSPFSCMDLTYVSLLLQEFGFPRS 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAGVGLIDAEKGGSLVVGDFEIAAKYVCRTLETQPQSSPFSCMDLTYVSLLLQEFGFPRS 420

Qy        421 KVLKLTRKIDNVETSWALGAIFHYIDSLNRQKSPAS 456
              ||||||||||||||||||||||||||||||||||||
Db        421 KVLKLTRKIDNVETSWALGAIFHYIDSLNRQKSPAS 456
```

```
RESULT 3
AAB72241
ID   AAB72241 standard; protein; 484 AA.
XX
AC   AAB72241;
XX
DT   14-MAY-2001  (first entry)
XX
DE   Human CD39 like protein CD39-L2 amino acid sequence.
XX
KW   Human CD39-like protein; apyrase; NDPase; platelet function inhibitor;
KW   myocardial infarction; cerebral ischaemia; angina; arterial thrombosis;
KW   cerebral artery thrombosis; platelet aggregation; inflammation;
KW   apoptosis; autoimmune disorder; neurological disorder;
KW   Alzheimer's disease; Parkinson's disease; cancer; CD39-L2.
XX
OS   Homo sapiens.
XX
PN   WO200110205-A1.
XX
PD   15-FEB-2001.
XX
PF   09-AUG-2000; 2000WO-US021790.
XX
PR   09-AUG-1999;   99US-00370265.
PR   11-JAN-2000; 2000US-00481238.
PR   25-APR-2000; 2000US-00557800.
PR   26-MAY-2000; 2000US-00583231.
PR   30-JUN-2000; 2000US-00608285.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Ford J,  Mulero JJ,  Yeung G;
XX
DR   WPI; 2001-147489/15.
DR   N-PSDB; AAF63386.
XX
PT   Polynucleotides encoding human CD39-like polypeptides, with apyrase
PT   and/or NDPase activity, which are useful in the treatment of pathological
PT   conditions caused by thrombosis (e.g. myocardial infarction) and
PT   inflammatory disorders.
XX
PS   Claim 39; Page 162-164; 203pp; English.
XX
CC   This invention relates to polynucleotides encoding human CD39-like
CC   polypeptides with apyrase and/or NDPase activity. The polypeptides having
CC   ATPDase, including NDPase, activity are useful for inhibiting platelet
CC   function and can therefore be used in the prophylaxis or treatment of
CC   pathological conditions caused by or involving thrombosis or excessive
CC   coagulation or excessive platelet aggregation, such as myocardial
CC   infarction, cerebral ischaemia, angina, arterial thrombosis, cerebral
CC   artery thrombosis or intracardiac thrombosis, and conditions associated
CC   with venous thrombosis. CD39-L4 and CD39-L2 polypeptides are useful in
CC   modulating disease states (including platelet aggregation, inflammation
CC   and apoptosis) associated with ADP or other purinergic signalling by
CC   reducing the levels of NDPs. The polypeptides are also useful for
CC   prophylaxis or treatment of inflammation related disorders, such as
CC   disorders involving sepsis or systemic inflammatory response syndrome or
CC   SIRS (and associated conditions such as fever, tachycardia, tachypnea,
CC   cytokine overstimulation); autoimmune disorders such as thrombosis,
CC   atherosclerosis, acute pancreatitis, dermatitis, including psoriasis,
CC   cirrhosis, reperfusion injury, asthma, multiple sclerosis, arthritis;
CC   neurological disorders including neurodegenerative diseases, epilepsy,
CC   depression, Alzheimer's disease, Parkinson's disease, Huntington's
CC   disease, and amyotrophic lateral sclerosis; and cancer. The present
CC   sequence represents human CD39 like protein CD39-L2
XX
SQ   Sequence 484 AA;

  Query Match             100.0%;  Score 2364;  DB 4;  Length 484;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-215;
  Matches  456;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRKISNHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRATATQAFFSITRAAPGARWGQQAH 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         29 MRKISNHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRATATQAFFSITRAAPGARWGQQAH 88

Qy         61 SPLGTAADGHEVFYGIMFDAGSTGTRVHVFQFTRPPRETPTLTHETFKAVKPGLSAYADD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         89 SPLGTAADGHEVFYGIMFDAGSTGTRVHVFQFTRPPRETPTLTHETFKAVKPGLSAYADD 148

Qy        121 VEKSAQGIRELLDVAKQDIPFDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASP 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        149 VEKSAQGIRELLDVAKQDIPFDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASP 208

Qy        181 FLVGDDCVSIMNGTDEGVSAWITINFLTGSLKTPGGSSVGMLDLGGGSTQIAFLPRVEGT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        209 FLVGDDCVSIMNGTDEGVSAWITINFLTGSLKTPGGSSVGMLDLGGGSTQIAFLPRVEGT 268

Qy        241 LQASPPGYLTALRMFNRTYKLYSYSYLGLGLMSARLAILGGVEGQPAKDGKELVSPCLSP 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        269 LQASPPGYLTALRMFNRTYKLYSYSYLGLGLMSARLAILGGVEGQPAKDGKELVSPCLSP 328

Qy        301 SFKGEWEHAEVTYRVSGQKAAASLHELCAARVSEVLQNRVHRTEEVKHVDFYAFSYYYDL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        329 SFKGEWEHAEVTYRVSGQKAAASLHELCAARVSEVLQNRVHRTEEVKHVDFYAFSYYYDL 388

Qy        361 AAGVGLIDAEKGGSLVVGDFEIAAKYVCRTLETQPQSSPFSCMDLTYVSLLLQEFGFPRS 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        389 AAGVGLIDAEKGGSLVVGDFEIAAKYVCRTLETQPQSSPFSCMDLTYVSLLLQEFGFPRS 448

Qy        421 KVLKLTRKIDNVETSWALGAIFHYIDSLNRQKSPAS 456
              ||||||||||||||||||||||||||||||||||||
Db        449 KVLKLTRKIDNVETSWALGAIFHYIDSLNRQKSPAS 484
```

```
RESULT 4
ADQ99473
ID   ADQ99473 standard; protein; 484 AA.
XX
AC   ADQ99473;
XX
DT   23-SEP-2004  (first entry)
XX
DE   Human CD39-like protein, CD39L2.
XX
KW   CD39-like protein; gene mapping; molecular weight marker;
KW   food supplement; anti-thrombotic; anti-tissue graft rejection agent;
KW   ATP neurotransmission; ecto-ATPase activity; nucleotide triphosphatase;
KW   NTPase; human; enzyme.
XX
OS   Homo sapiens.
XX
```

PN US6759214-B1.
XX
PD 06-JUL-2004.
XX
PF 13-JUL-2001; 2001US-00908510.
XX
PR 29-JAN-1999; 99US-00240639.
XX
PA (NUVE-) NUVELO INC.
XX
PI Chadwick BP, Frischauf A;
XX
DR WPI; 2004-515395/49.
DR N-PSDB; ADQ99441, ADQ99441.
XX
PT New CD-39-like polypeptides and polynucleotides, useful in chromosome and
PT gene mapping, as molecular weight markers, as food supplements, or as
PT anti-thrombotic or anti-tissue graft rejection agents.
XX
PS Claim 2; Fig 8A-D; 104pp; English.
XX
CC The invention relates to novel CD39-like polypeptides (CD39-like
CC nucleotide triphosphatase; NTPase) and nucleic acid molecules encoding
CC such polypeptides. CD39-like polynucleotides may be used as hybridisation
CC probes, PCR primers and in chromosome and gene mapping. Polypeptides of
CC the invention may be used as molecular weight markers, as food
CC supplements, in generating an antibody that specifically binds the
CC polypeptide, as anti-thrombotic or anti-tissue graft rejection agents, or
CC for regulating ATP neurotransmission in smooth muscle, peripheral ganglia
CC or brain. Sequences of the invention are useful in modulating ecto-ATPase
CC activity and for identifying compounds that modulate ecto-ATPase
CC activity. The present sequence is human CD39-like protein, CD39L2. Note:
CC This sequence is stated to be the same as that shown in SEQ ID 2 of the
CC sequence listing, however this sequence is longer at the N-terminal. The
CC shorter sequence is represented in ADQ99442.
XX
SQ Sequence 484 AA;

Query Match 100.0%; Score 2364; DB 8; Length 484;
Best Local Similarity 100.0%; Pred. No. 1.3e-215;
Matches 456; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MRKISNHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRATATQAFFSITRAAPGARWGQQAH 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         29 MRKISNHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRATATQAFFSITRAAPGARWGQQAH 88

Qy         61 SPLGTAADGHEVFYGIMFDAGSTGTRVHVFQFTRPPRETPTLTHETFKAVKPGLSAYADD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         89 SPLGTAADGHEVFYGIMFDAGSTGTRVHVFQFTRPPRETPTLTHETFKAVKPGLSAYADD 148

Qy        121 VEKSAQGIRELLDVAKQDIPFDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASP 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        149 VEKSAQGIRELLDVAKQDIPFDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASP 208

Qy        181 FLVGDDCVSIMNGTDEGVSAWITINFLTGSLKTPGGSSVGMLDLGGGSTQIAFLPRVEGT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        209 FLVGDDCVSIMNGTDEGVSAWITINFLTGSLKTPGGSSVGMLDLGGGSTQIAFLPRVEGT 268

Qy        241 LQASPPGYLTALRMFNRTYKLYSYSYLGLGLMSARLAILGGVEGQPAKDGKELVSPCLSP 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        269 LQASPPGYLTALRMFNRTYKLYSYSYLGLGLMSARLAILGGVEGQPAKDGKELVSPCLSP 328

Qy        301 SFKGEWEHAEVTYRVSGQKAAASLHELCAARVSEVLQNRVHRTEEVKHVDFYAFSYYYDL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        329 SFKGEWEHAEVTYRVSGQKAAASLHELCAARVSEVLQNRVHRTEEVKHVDFYAFSYYYDL 388

Qy        361 AAGVGLIDAEKGGSLVVGDFEIAAKYVCRTLETQPQSSPFSCMDLTYVSLLLQEFGFPRS 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        389 AAGVGLIDAEKGGSLVVGDFEIAAKYVCRTLETQPQSSPFSCMDLTYVSLLLQEFGFPRS 448

Qy        421 KVLKLTRKIDNVETSWALGAIFHYIDSLNRQKSPAS 456
              ||||||||||||||||||||||||||||||||||||
Db        449 KVLKLTRKIDNVETSWALGAIFHYIDSLNRQKSPAS 484
```

RESULT 5
ABB06124
ID ABB06124 standard; protein; 463 AA.
XX
AC ABB06124;
XX
DT 10-MAY-2002 (first entry)
XX
DE Human NS protein sequence SEQ ID NO:216.
XX
KW Human; cytostatic; osteopathic; gynaecological; neuroprotective;
KW antirheumatic; antiarthritic; antipsoriatic; ophthalmological; anti-HIV;
KW vasotropic; antiarteriosclerotic; antiinflammatory; dermatological;
KW anorectic; muscular; antiinfertility; cardiovascular; anticoagulant;
KW antifibrinolytic; hypotension; antiasthmatic; immunomodulator; cardiant;
KW anticonvulsant; antidiabetic; tranquilliser; antidepressant; aeuroleptic;
KW gastrointestinal; virucide; antiulcer; cerebroprotective; nootropic;
KW contraceptive; vaccine; gene therapy; cancer; osteoporosis; dystonia;
KW endometriosis; degenerative disease; multiple sclerosis; psoriasis;
KW rheumatoid arthritis; cataract; restenosis; atherosclerosis; glaucoma;
KW inflammation; skin disorder; obesity; muscular dystrophy; AIDS;
KW infertility; cardiovascular disease; coagulation disease; hypertension;
KW ischaemia; asthma; immune disease; epilepsy; angina; neurodegeneration;
KW diabetes; anxiety; depression; schizophrenia; viral disease; stroke;
KW gastric ulcer; Alzheimer's disease.
XX
OS Homo sapiens.
XX
PN WO200206315-A2.
XX
PD 24-JAN-2002.
XX
PF 17-JUL-2001; 2001WO-IL000653.
XX
PR 18-JUL-2000; 2000IL-00137345.
PR 15-DEC-2000; 2000IL-00140354.
XX
PA (COMP-) COMPUGEN LTD.
XX
PI Mintz L, Freilich S, Bernstein J;
XX
DR WPI; 2002-155037/20.
DR N-PSDB; ABL39778.
XX
PT One hundred and twenty eight novel nucleic acid sequences, useful for
PT treating and diagnosing e.g. cancer, asthma and Alzheimer's.
XX
PS Claim 6; Page 251-253; 290pp; English.
XX
CC ABL39691 to ABL39818 represent novel human nucleic acid sequences
CC encoding the proteins given in ABB06037 to ABB06164. The novel sequences
CC (NS) can have cytostatic, osteopathic, gynaecological, neuroprotective,
CC antirheumatic, antiarthritic, antipsoriatic, ophthalmological, virucide,
CC vasotropic, antiarteriosclerotic, antiinflammatory, dermatological,
CC anorectic, muscular, anti-HIV, antiinfertility, cardiovascular,
CC anticoagulant, antifibrinolytic, hypotension, antiasthmatic, cardiant,
CC immunomodulator, anticonvulsant, antidiabetic, tranquilliser, antiulcer,
CC antidepressant, gastrointestinal, aeuroleptic, cerebroprotective,
CC nootropic and contraceptive activities. The NS can be used in vaccines,
CC gene therapy and antisense therapy. Nucleic acids, expression vectors and
CC antibodies from the present invention can be used for treating and
CC diagnosing e.g. cancer, osteoporosis, endometriosis, degenerative
CC diseases, dystonia, multiple sclerosis, rheumatoid arthritis, psoriasis,
CC cataracts, restenosis, atherosclerosis, inflammation, skin disorders,
CC glaucoma, obesity, muscular dystrophy, AIDS, infertility, cardiovascular
CC disease, coagulation disease, ischaemia, hypertension, asthma, immune
CC disease, epilepsy, angina, neurodegeneration, diabetes, anxiety,
CC depression, schizophrenia, viral disease, gastric ulcers, stroke,
CC Alzheimer's disease and as a contraceptive
XX
SQ Sequence 463 AA;

```
  Query Match             99.9%;  Score 2361;  DB 5;  Length 463;
  Best Local Similarity   99.8%;  Pred. No. 2.3e-215;
  Matches  455;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRKISNHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRATATQAFFSITRAAPGARWGQQAH 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          8 MRKISNHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRATATQAFFSITRAAPGARWGQQAH 67

Qy         61 SPLGTAADGHEVFYGIMFDAGSTGTRVHVFQFTRPPRETPTLTHETFKAVKPGLSAYADD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||:||||||||||
Db         68 SPLGTAADGHEVFYGIMFDAGSTGTRVHVFQFTRPPRETPTLTHETFKALKPGLSAYADD 127

Qy        121 VEKSAQGIRELLDVAKQDIPFDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASP 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        128 VEKSAQGIRELLDVAKQDIPFDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASP 187

Qy        181 FLVGDDCVSIMNGTDEGVSAWITINFLTGSLKTPGGSSVGMLDLGGGSTQIAFLPRVEGT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        188 FLVGDDCVSIMNGTDEGVSAWITINFLTGSLKTPGGSSVGMLDLGGGSTQIAFLPRVEGT 247

Qy        241 LQASPPGYLTALRMFNRTYKLYSYSYLGLGLMSARLAILGGVEGQPAKDGKELVSPCLSP 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        248 LQASPPGYLTALRMFNRTYKLYSYSYLGLGLMSARLAILGGVEGQPAKDGKELVSPCLSP 307

Qy        301 SFKGEWEHAEVTYRVSGQKAAASLHELCAARVSEVLQNRVHRTEEVKHVDFYAFSYYYDL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        308 SFKGEWEHAEVTYRVSGQKAAASLHELCAARVSEVLQNRVHRTEEVKHVDFYAFSYYYDL 367

Qy        361 AAGVGLIDAEKGGSLVVGDFEIAAKYVCRTLETQPQSSPFSCMDLTYVSLLLQEFGFPRS 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        368 AAGVGLIDAEKGGSLVVGDFEIAAKYVCRTLETQPQSSPFSCMDLTYVSLLLQEFGFPRS 427

Qy        421 KVLKLTRKIDNVETSWALGAIFHYIDSLNRQKSPAS 456
              ||||||||||||||||||||||||||||||||||||
Db        428 KVLKLTRKIDNVETSWALGAIFHYIDSLNRQKSPAS 463
```

```
RESULT 6
ABJ04657
ID   ABJ04657 standard; protein; 467 AA.
XX
AC   ABJ04657;
XX
DT   11-OCT-2002  (first entry)
XX
DE   Protein of NOVX 15a SEQ ID No 36.
XX
KW   Cytostatic; antidiabetic; anorectic; metabolic; nootropic; antilipaemic;
KW   neuroprotective; antiparkinsonian; anticonvulsant; cerebroprotective;
KW   tranquiliser; neuroleptic; antidiabetic; antiulcer; antiinflammatory;
KW   anti-HIV; antiallergic; antirheumatic; antiarthritic; NOVX; diabetes;
KW   metabolic disorder; obesity; infectious disease; Alzheimer's disease;
KW   anorexia; neurodegenerative disorder; Parkinson's disorder; obesity;
KW   immune disorder; haematopoietic disorder; dyslipidaemia; chronic disease;
KW   metabolic syndrome X; wasting disorder; cancer; neurological disorder;
KW   epilepsy; stroke; mental disorder; schizophrenic disorders; goiter;
KW   vesicular transport; cystic fibrosis; gastrointestinal disorder;
KW   diabetes mellitus; ulcerative colitis; AIDS; allergic reaction;
KW   multiple sclerosis; rheumatoid arthritis; transgenic animal;
KW   gene therapy.
XX
OS   Unidentified.
XX
PN   WO200246409-A2.
XX
PD   13-JUN-2002.
XX
PF   06-DEC-2001; 2001WO-US046586.
XX
PR   06-DEC-2000; 2000US-0251660P.
PR   12-DEC-2000; 2000US-0255029P.
PR   08-JAN-2001; 2001US-0260326P.
PR   24-JAN-2001; 2001US-0263800P.
PR   20-FEB-2001; 2001US-0269942P.
PR   24-APR-2001; 2001US-0286183P.
PR   20-AUG-2001; 2001US-0313627P.
PR   12-SEP-2001; 2001US-0318712P.
XX
PA   (CURA-) CURAGEN CORP.
XX
PI   Guo X,  Li L,  Patturajan M,  Shimkets RA,  Casman SJ,  Malyankar UM;
PI   Tchernev VT,  Vernet CAM,  Spytek KA,  Shenoy SG,  Alsobrook JP;
PI   Edinger S,  Peyman JA,  Stone DJ,  Ellerman K,  Gangolli EA,  Boldog FL;
PI   Colman SD,  Eisen AJ,  Liu X,  Padigaru M,  Spaderna SK,  Zerhusen BD;
XX
DR   WPI; 2002-547774/58.
DR   N-PSDB; ABT05470.
XX
PT   Novel isolated polypeptide, designated NOVX, useful for treating or
PT   preventing cancer, diabetes, obesity, dyslipidemia, anorexia, and
PT   metabolic, neurodegenerative, immune and hematopoietic disorders.
XX
PS   Claim 1; Page 140; 421pp; English.
XX
CC   The invention relates to an isolated polypeptide, designated NOVX,
CC   comprising a sequence fully defined in the specification. The isolated
CC   protein, its encoding polynucleotide or an antibody created from the
CC   protein is useful in the manufacture of a medicament for treating a
CC   syndrome associated with a human disease, preferably a NOVX-associated
CC   disorder, or for treating or preventing a NOVX-associated disorder in a
CC   subject, preferably human. The isolated protein, its encoding
CC   polynucleotide or an antibody created from the protein are also useful
CC   for treating or preventing metabolic disorders, diabetes, obesity,
CC   infectious disease, anorexia, neurodegenerative disorder, Alzheimer's
CC   disease, Parkinson's disorder, immune disorders, haematopoietic
CC   disorders, and various dyslipidaemias, metabolic disturbances associated
CC   with obesity, the metabolic syndrome X, wasting disorders associated with
CC   chronic diseases, and cancer. The isolated protein, its encoding
CC   polynucleotide or an antibody created from the protein are useful for
CC   treating or preventing neurological disorders such as epilepsy, stroke,
CC   mental disorders including mood, anxiety, schizophrenic disorders,
CC   disorders of vesicular transport such as cystic fibrosis, diabetes
CC   mellitus, goiter, gastrointestinal disorders including ulcerative
CC   colitis, other conditions associated with abnormal vesicle trafficking
CC   including AIDS, allergic reactions, multiple sclerosis and rheumatoid
CC   arthritis. A cell comprising the vector of the invention is useful for
CC   producing non-human transgenic animals. The polynucleotide of the
CC   invention can be used to treat disorders by gene therapy. This sequence
CC   represents one of the isolated NOVX proteins of the invention
XX
SQ   Sequence 467 AA;
```

```
  Query Match             99.9%;  Score 2361;  DB 5;  Length 467;
  Best Local Similarity   99.8%;  Pred. No. 2.4e-215;
  Matches  455;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRKISNHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRATATQAFFSITRAAPGARWGQQAH 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         12 MRKISNHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRATATQAFFSITRAAPGARWGQQAH 71

Qy         61 SPLGTAADGHEVFYGIMFDAGSTGTRVHVFQFTRPPRETPTLTHETFKAVKPGLSAYADD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||:||||||||||
Db         72 SPLGTAADGHEVFYGIMFDAGSTGTRVHVFQFTRPPRETPTLTHETFKALKPGLSAYADD 131

Qy        121 VEKSAQGIRELLDVAKQDIPFDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASP 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        132 VEKSAQGIRELLDVAKQDIPFDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASP 191

Qy        181 FLVGDDCVSIMNGTDEGVSAWITINFLTGSLKTPGGSSVGMLDLGGGSTQIAFLPRVEGT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        192 FLVGDDCVSIMNGTDEGVSAWITINFLTGSLKTPGGSSVGMLDLGGGSTQIAFLPRVEGT 251

Qy        241 LQASPPGYLTALRMFNRTYKLYSYSYLGLGLMSARLAILGGVEGQPAKDGKELVSPCLSP 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        252 LQASPPGYLTALRMFNRTYKLYSYSYLGLGLMSARLAILGGVEGQPAKDGKELVSPCLSP 311
```

```
Qy        301 SFKGEWEHAEVTYRVSGQKAAASLHELCAARVSEVLQNRVHRTEEVKHVDFYAFSYYYDL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        312 SFKGEWEHAEVTYRVSGQKAAASLHELCAARVSEVLQNRVHRTEEVKHVDFYAFSYYYDL 371

Qy        361 AAGVGLIDAEKGGSLVVGDFEIAAKYVCRTLETQPQSSPFSCMDLTYVSLLLQEFGFPRS 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        372 AAGVGLIDAEKGGSLVVGDFEIAAKYVCRTLETQPQSSPFSCMDLTYVSLLLQEFGFPRS 431

Qy        421 KVLKLTRKIDNVETSWALGAIFHYIDSLNRQKSPAS 456
              |||||||||||||||||||||||||||||||||||
Db        432 KVLKLTRKIDNVETSWALGAIFHYIDSLNRQKSPAS 467
```

RESULT 7
AAM93929
ID AAM93929 standard; protein; 456 AA.
XX
AC AAM93929;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human polypeptide, SEQ ID NO: 4100.
XX
KW Human; full length cDNA; cDNA synthesis; oligo-capping.
XX
OS Homo sapiens.
XX
PN EP1130094-A2.
XX
PD 05-SEP-2001.
XX
PF 07-JUL-2000; 2000EP-00114089.
XX
PR 08-JUL-1999; 99JP-00194486.
PR 11-JAN-2000; 2000JP-00118774.
PR 02-MAY-2000; 2000JP-00183765.
XX
PA (HELI-) HELIX RES INST.
XX
PI Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
XX
DR WPI; 2001-524255/58.
DR N-PSDB; AAK94892.
XX
PT 830 Primers useful for synthesizing full length cDNA clones and their use
PT in genetic manipulation.
XX
PS Claim 8; SEQ ID NO 4100; 1380pp + Sequence Listing; English.
XX
CC The invention relates to primers for synthesising full length cDNA
CC clones. 830 cDNA molecules encoding a human protein have been isolated
CC and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have
CC been determined. Primers for synthesising the full length cDNA are useful
CC for clarifying the function of the protein encoded by the cDNA. The full
CC length clones were obtained by construction of full length enriched cDNA
CC libraries that were synthesised by the oligo-capping method. The primers
CC enable the production of the full length cDNA easily without any special
CC methods. The present sequence is a polypeptide encoded by a full length
CC human cDNA of the invention. Note: The sequence data for this patent did
CC not form part of the printed specification, but was obtained in CD-ROM
CC format directly from EPO
XX
SQ Sequence 456 AA;

Query Match 99.5%; Score 2351; DB 4; Length 456;
Best Local Similarity 99.3%; Pred. No. 2e-214;
Matches 453; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```
Qy          1 MRKISNHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRATATQAFFSITRAAPGARWGQQAH 60
              |||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db          1 MRKISNHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRATAIQAFFSITRAAPGARWGQQAH 60

Qy         61 SPLGTAADGHEVFYGIMFDAGSTGTRVHVFQFTRPPRETPTLTHETFKAVKPGLSAYADD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||:||||||||
Db         61 SPLGTAADGHEVFYGIMFDAGSTGTRVHVFQFTRPPRETPTLTHETFKALKPGLSAYADD 120

Qy        121 VEKSAQGIRELLDVAKQDIPFDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASP 180
              ||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db        121 VEKSAQGIRELLDVAKQDIPFDFWKATPLVLKATVGLRLLPGEKAQKLLQKVKEVFKASP 180

Qy        181 FLVGDDCVSIMNGTDEGVSAWITINFLTGSLKTPGGSSVGMLDLGGGSTQIAFLPRVEGT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 FLVGDDCVSIMNGTDEGVSAWITINFLTGSLKTPGGSSVGMLDLGGGSTQIAFLPRVEGT 240

Qy        241 LQASPPGYLTALRMFNRTYKLYSYSYLGLGLMSARLAILGGVEGQPAKDGKELVSPCLSP 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 LQASPPGYLTALRMFNRTYKLYSYSYLGLGLMSARLAILGGVEGQPAKDGKELVSPCLSP 300

Qy        301 SFKGEWEHAEVTYRVSGQKAAASLHELCAARVSEVLQNRVHRTEEVKHVDFYAFSYYYDL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 SFKGEWEHAEVTYRVSGQKAAASLHELCAARVSEVLQNRVHRTEEVKHVDFYAFSYYYDL 360

Qy        361 AAGVGLIDAEKGGSLVVGDFEIAAKYVCRTLETQPQSSPFSCMDLTYVSLLLQEFGFPRS 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAGVGLIDAEKGGSLVVGDFEIAAKYVCRTLETQPQSSPFSCMDLTYVSLLLQEFGFPRS 420

Qy        421 KVLKLTRKIDNVETSWALGAIFHYIDSLNRQKSPAS 456
              |||||||||||||||||||||||||||||||||||
Db        421 KVLKLTRKIDNVETSWALGAIFHYIDSLNRQKSPAS 456
```

RESULT 8
ADL32067
ID ADL32067 standard; protein; 456 AA.
XX
AC ADL32067;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human protein encoded by a full length cDNA clone SeqID 4100.
XX
KW human; medicine; signal transduction; glycoprotein; transcription;
KW oligo-capping method.
XX
OS Homo sapiens.
XX
PN EP1396543-A2.
XX
PD 10-MAR-2004.
XX
PF 07-JUL-2000; 2003EP-00025638.
XX
PR 08-JUL-1999; 99JP-00194486.
PR 11-JAN-2000; 2000JP-00118774.
PR 02-MAY-2000; 2000JP-00183865.
PR 07-JUL-2000; 2000EP-00114089.
XX
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
XX
PI Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
XX
DR WPI; 2004-204755/20.
DR N-PSDB; ADL32066.
XX
PT New oligonucleotide primers (830 cDNAs) useful for synthesizing full
PT length human cDNAs.
XX
PS Example 1; SEQ ID NO 4100; 1340pp; English.
XX
CC This invention relates to a novel primers useful for synthesising full
CC length cDNA molecules that encode human proteins. Specifically, it refers
CC to secretory or membrane proteins that are potential therapeutic agents/
CC target molecules in the field of medicine, and in particular genes

```
CC   encoding proteins that are associated with signal transduction,
CC   glycoproteins and transcription. The present invention describes a method
CC   for efficiently cloning a full length human cDNA from both the 5' and 3'
CC   ends using the oligo-capping method. This polypeptide sequence is a full
CC   length human protein of the invention.
XX
SQ   Sequence 456 AA;

  Query Match             99.5%;  Score 2351;  DB 8;  Length 456;
  Best Local Similarity   99.3%;  Pred. No. 2e-214;
  Matches  453;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 MRKISNHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRATATQAFFSITRAAPGARWGQQAH 60
              ||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db          1 MRKISNHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRATAIQAFFSITRAAPGARWGQQAH 60

Qy         61 SPLGTAADGHEVFYGIMFDAGSTGTRVHVFQFTRPPRETPTLTHETFKAVKPGLSAYADD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||:||||||||||
Db         61 SPLGTAADGHEVFYGIMFDAGSTGTRVHVFQFTRPPRETPTLTHETFKALKPGLSAYADD 120

Qy        121 VEKSAQGIRELLDVAKQDIPFDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASP 180
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db        121 VEKSAQGIRELLDVAKQDIPFDFWKATPLVLKATVGLRLLPGEKAQKLLQKVKEVFKASP 180

Qy        181 FLVGDDCVSIMNGTDEGVSAWITINFLTGSLKTPGGSSVGMLDLGGGSTQIAFLPRVEGT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 FLVGDDCVSIMNGTDEGVSAWITINFLTGSLKTPGGSSVGMLDLGGGSTQIAFLPRVEGT 240

Qy        241 LQASPPGYLTALRMFNRTYKLYSYSYLGLGLMSARLAILGGVEGQPAKDGKELVSPCLSP 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 LQASPPGYLTALRMFNRTYKLYSYSYLGLGLMSARLAILGGVEGQPAKDGKELVSPCLSP 300

Qy        301 SFKGEWEHAEVTYRVSGQKAAASLHELCAARVSEVLQNRVHRTEEVKHVDFYAFSYYYDL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 SFKGEWEHAEVTYRVSGQKAAASLHELCAARVSEVLQNRVHRTEEVKHVDFYAFSYYYDL 360

Qy        361 AAGVGLIDAEKGGSLVVGDFEIAAKYVCRTLETQPQSSPFSCMDLTYVSLLLQEFGFPRS 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAGVGLIDAEKGGSLVVGDFEIAAKYVCRTLETQPQSSPFSCMDLTYVSLLLQEFGFPRS 420

Qy        421 KVLKLTRKIDNVETSWALGAIFHYIDSLNRQKSPAS 456
              ||||||||||||||||||||||||||||||||||||
Db        421 KVLKLTRKIDNVETSWALGAIFHYIDSLNRQKSPAS 456


RESULT 9
ADC14220
ID   ADC14220 standard; protein; 450 AA.
XX
AC   ADC14220;
XX
DT   18-DEC-2003  (first entry)
XX
DE   Human enzyme ENZM-26.
XX
KW   enzyme; human; ENZM; cytostatic; antiarteriosclerotic; antidiabetic;
KW   anticonvulsant; nootropic; neuroprotective; cerebroprotective; anti-HIV;
KW   antiallergic; antiinflammatory; thyromimetic; gene therapy;
KW   cell proliferative disorder; endocrine disorder; neurological disorder;
KW   immune system disorder; inflammatory disorder; developmental disorder;
KW   reproductive disorder; vesicle-trafficking disorder; infection.
XX
OS   Homo sapiens.
XX
PN   WO2003042357-A2.
XX
PD   22-MAY-2003.
XX
PF   26-SEP-2002; 2002WO-US031096.
XX
PR   28-SEP-2001; 2001US-0326388P.
PR   12-OCT-2001; 2001US-0328979P.
PR   19-OCT-2001; 2001US-0346034P.
PR   26-OCT-2001; 2001US-0348284P.
PR   08-NOV-2001; 2001US-0338048P.
PR   16-NOV-2001; 2001US-0332340P.
PR   14-DEC-2001; 2001US-0340357P.
PR   29-MAR-2002; 2002US-0368722P.
PR   29-MAR-2002; 2002US-0368799P.
PR   17-MAY-2002; 2002US-0381558P.
PR   07-JUN-2002; 2002US-0387119P.
PR   21-JUN-2002; 2002US-0390662P.
XX
PA   (INCY-) INCYTE GENOMICS INC.
XX
PI   Yang J,  Lu DAM,  Yue H,  Elliott VS,  Warren BA,  Duggan BM;
PI   Forsythe IJ,  Lee EA,  Hafalia AJA,  Ramkumar J,  Chawla NK,  Baughn MR;
PI   Becha SD,  Gorvad AE,  Tran UK,  Li JX,  Yao MG,  Ison CH,  Griffin JA;
PI   Lee SY,  Chang H,  Emerling BM,  Tang YT,  Lal PG,  Kable AE;
PI   Marquis JP,  Jiang X,  Jackson AA,  Zebarjadian Y,  Swarnakar A;
PI   Wilson AD,  Jin P,  Richardson TW,  Bhatia U,  Burrill JD,  Lee S;
PI   Blake JJ,  Ho A,  Zheng W,  Gao J;
XX
DR   WPI; 2003-449567/42.
DR   N-PSDB; ADC14273.
XX
PT   New human enzymes (ENZM), useful for diagnosing, treating and preventing
PT   diseases or conditions associated with the aberrant ENZM expression e.g.
PT   cancer, diabetes, epilepsy, or infections.
XX
PS   Claim 1; SEQ ID NO 26; 416pp; English.
XX
CC   The invention relates to a novel isolated human enzyme (ENZM)
CC   polypeptide. A polypeptide of the invention has cytostatic,
CC   antiarteriosclerotic, antidiabetic, anticonvulsant, nootropic,
CC   neuroprotective, cerebroprotective, anti-HIV, antiallergic,
CC   antiinflammatory, and thyromimetic activity. A polynucleotide encoding a
CC   polypeptide of the invention may have a use in gene therapy. The
CC   polypeptides and polynucleotides are useful in diagnosing, treating and
CC   preventing diseases or conditions associated with the decreased
CC   expression or overexpression of ENZM, such as cell proliferative (e.g.
CC   cancer, atherosclerosis), endocrine (e.g. diabetes), neurological (e.g.
CC   epilepsy, Huntington's disease, stroke), immune/inflammatory (e.g. AIDS,
CC   allergies), developmental (e.g. Hypothyroidism, Cushing's syndrome),
CC   reproductive and vesicle-trafficking disorders, or infections. These are
CC   also useful in assessing the effects of exogenous compounds on the
CC   expression of nucleic acid and amino acid sequences of ENZM. The ENZM or
CC   its fragments are useful in screening compounds for effectiveness as
CC   agonist or antagonist of the polypeptides, or in altering the expression
CC   of the target polynucleotide and compounds that specifically bind to or
CC   modulate the activity of the polypeptide. The microarray is useful in
CC   monitoring or measuring protein-protein interactions, drug-target
CC   interactions, and gene expression profiles. The sequences shown in
CC   ADC14195-ADC14247 represent ENZM proteins of the invention.
XX
SQ   Sequence 450 AA;

  Query Match             91.0%;  Score 2152;  DB 7;  Length 450;
  Best Local Similarity   92.3%;  Pred. No. 1.7e-195;
  Matches  421;  Conservative    1;  Mismatches    0;  Indels   34;  Gaps    1;

Qy          1 MRKISNHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRATATQAFFSITRAAPGARWGQQAH 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         29 MRKISNHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRATATQAFFSITRAAPGARWGQQAH 88

Qy         61 SPLGTAADGHEVFYGIMFDAGSTGTRVHVFQFTRPPRETPTLTHETFKAVKPGLSAYADD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||:||||||||||
Db         89 SPLGTAADGHEVFYGIMFDAGSTGTRVHVFQFTRPPRETPTLTHETFKALKPGLSAYADD 148

Qy        121 VEKSAQGIRELLDVAKQDIPFDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASP 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        149 VEKSAQGIRELLDVAKQDIPFDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASP 208

Qy        181 FLVGDDCVSIMNGTDEGVSAWITINFLTGSLKTPGGSSVGMLDLGGGSTQIAFLPRVEGT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        209 FLVGDDCVSIMNGTDEGVSAWITINFLTGSLKTPGGSSVGMLDLGGGSTQIAFLPRVEGT 268
```

```
Qy        241 LQASPPGYLTALRMFNRTYKLYSYSYLGLGLMSARLAILGGVEGQPAKDGKELVSPCLSP 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        269 LQASPPGYLTALRMFNRTYKLYSYSYLGLGLMSARLAILGGVEGQP-------------- 314

Qy        301 SFKGEWEHAEVTYRVSGQKAAASLHELCAARVSEVLQNRVHRTEEVKHVDFYAFSYYYDL 360
                                  ||||||||||||||||||||||||||||||||||||||
Db        315 --------------------AASLHELCAARVSEVLQNRVHRTEEVKHVDFYAFSYYYDL 354

Qy        361 AAGVGLIDAEKGGSLVVGDFEIAAKYVCRTLETQPQSSPFSCMDLTYVSLLLQEFGFPRS 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        355 AAGVGLIDAEKGGSLVVGDFEIAAKYVCRTLETQPQSSPFSCMDLTYVSLLLQEFGFPRS 414

Qy        421 KVLKLTRKIDNVETSWALGAIFHYIDSLNRQKSPAS 456
              ||||||||||||||||||||||||||||||||||||
Db        415 KVLKLTRKIDNVETSWALGAIFHYIDSLNRQKSPAS 450
```

RESULT 10
AAU30882
ID AAU30882 standard; protein; 462 AA.
XX
AC AAU30882;
XX
DT 18-DEC-2001 (first entry)
XX
DE Novel human secreted protein #1373.
XX
KW Human; vaccination; gene therapy; nutritional supplement;
KW stem cell proliferation; haematopoiesis; nerve tissue regeneration;
KW immune suppression; immune stimulation; anti-inflammatory; leukaemia.
XX
OS Homo sapiens.
XX
PN WO200179449-A2.
XX
PD 25-OCT-2001.
XX
PF 16-APR-2001; 2001WO-US008656.
XX
PR 18-APR-2000; 2000US-00552929.
PR 26-JAN-2001; 2001US-00770160.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Drmanac RT;
XX
DR WPI; 2001-611725/70.
XX
PT Nucleic acids encoding a range of human polypeptides, useful in genetic
PT vaccination, testing and therapy.
XX
PS Claim 20; Page 365; 765pp; English.
XX
CC The invention relates to novel human secreted polypeptides. The
CC polypeptides and antibodies to the polypeptides are useful for
CC determining the presence of or predisposition to a disease associated
CC with altered levels of polypeptide. The polypeptides are also useful for
CC identifying agents (agonists and antagonists) that bind to them. Cells
CC expressing the proteins are useful for identifying a therapeutic agent
CC for use in treatment of a pathology related to aberrant expression or
CC physiological interactions of the polypeptide. Vectors comprising the
CC nucleic acids encoding the polypeptides and cells genetically engineered
CC to express them are also useful for producing the proteins. The proteins
CC are useful in genetic vaccination, testing and therapy, and can be used
CC as nutritional supplements. They may be used to increase stem cell
CC proliferation; to regulate haematopoiesis; and in bone, cartilage, tendon
CC and/or nerve tissue growth or regeneration; immune suppression and/or
CC stimulation; as anti-inflammatory agents; and in treatment of leukaemias.
CC AAU29510-AAU33304 represent the amino acid sequences of novel human
CC secreted proteins of the invention
XX
SQ Sequence 462 AA;

Query Match 90.3%; Score 2135; DB 4; Length 462;
Best Local Similarity 92.1%; Pred. No. 7.5e-194;
Matches 422; Conservative 2; Mismatches 8; Indels 26; Gaps 3;

```
Qy          1 MRKISNHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRATATQAFFSITRAAPGARWGQQAH 60
              ||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db         29 MRKISNHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRANATQAFFSITRAAPGARWGQQAH 88

Qy         61 SPLGTAADGHEVFYGIMFDAGSTGTRVHVFQFTRPPRETPTLTHETFKAVKPGLSAYADD 120
              |||||||||||||||||||||||||||||||||||||||||||||                ||||
Db         89 SPLGTAADGHEVFYGIMFDAGSTGTRVHVFQF----------------------------YADD 124

Qy        121 VEKSAQGIRELLDVAKQDIPFDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASP 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        125 VEKSAQGIRELLDVAKQDIPFDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASP 184

Qy        181 FLVGDDCVSIMNGTDEGVSAWITINFLTGSLKTPGGSSVGMLDLGGGSTQIAFLPRVEGT 240
              ||||||||||||||:||||||||||||||||||  |:|||||||||||||  ||  ||||
Db        185 FLVGDDCVSIMNGTNEGVSAWITINFLTGSLKTPRRSNVGMLDLGGGSTQIVFLTHVEGT 244

Qy        241 LQASPPGYLTALRMFNRTYKLYSYSYLGLGLMSARLAILGGVEGQPAKDGKELVSPCLSP 300
              |||||| |||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db        245 LQASPPRYLTALRMFNRTYKLYCYSYLGLGLMSARLAILGGVEGQPAKDGKELVSPCLSP 304

Qy        301 SFKGEWEHAEVTYRVSGQKAAASLHELCAARVSEVLQNRVHRTEEVKHVDFYAFSYYYDL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        305 SFKGEWEHAEVTYRVSGQKAAASLHELCAARVSEVLQNRVHRTEEVKHVDFYAFSYYYDL 364

Qy        361 AAGVGLIDAEKGGSLVVGDFEIAAKYVC-RTL-ETQPQSSPFSCMDLTYVSLLLQEFGFP 418
              |||||||||||||||||||||||||||| ||| |||||||||||||||||||||||||||||
Db        365 AAGVGLIDAEKGGSLVVGDFEIAAKYVCVRTLGETQPQSSPFSCMDLTYVSLLLQEFGFP 424

Qy        419 RSKVLKLTRKIDNVETSWALGAIFHYIDSLNRQKSPAS 456
              ||||||||||||||||||||||||||||||||||||||
Db        425 RSKVLKLTRKIDNVETSWALGAIFHYIDSLNRQKSPAS 462
```

RESULT 11
ABJ04658
ID ABJ04658 standard; protein; 446 AA.
XX
AC ABJ04658;
XX
DT 11-OCT-2002 (first entry)
XX
DE Protein of NOVX 15b SEQ ID No 38.
XX
KW Cytostatic; antidiabetic; anorectic; metabolic; nootropic; antilipaemic;
KW neuroprotective; antiparkinsonian; anticonvulsant; cerebroprotective;
KW tranquiliser; neuroleptic; antidiabetic; antiulcer; antiinflammatory;
KW anti-HIV; antiallergic; antirheumatic; antiarthritic; NOVX; diabetes;
KW metabolic disorder; obesity; infectious disease; Alzheimer's disease;
KW anorexia; neurodegenerative disorder; Parkinson's disorder; obesity;
KW immune disorder; haematopoietic disorder; dyslipidaemia; chronic disease;
KW metabolic syndrome X; wasting disorder; cancer; neurological disorder;
KW epilepsy; stroke; mental disorder; schizophrenic disorders; goiter;
KW vesicular transport; cystic fibrosis; gastrointestinal disorder;
KW diabetes mellitus; ulcerative colitis; AIDS; allergic reaction;
KW multiple sclerosis; rheumatoid arthritis; transgenic animal;
KW gene therapy.
XX
OS Unidentified.
XX
PN WO200246409-A2.
XX
PD 13-JUN-2002.
XX
PF 06-DEC-2001; 2001WO-US046586.
XX
PR 06-DEC-2000; 2000US-0251660P.
PR 12-DEC-2000; 2000US-0255029P.
PR 08-JAN-2001; 2001US-0260326P.

PR 24-JAN-2001; 2001US-0263800P.
PR 20-FEB-2001; 2001US-0269942P.
PR 24-APR-2001; 2001US-0286183P.
PR 20-AUG-2001; 2001US-0313627P.
PR 12-SEP-2001; 2001US-0318712P.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Guo X, Li L, Patturajan M, Shimkets RA, Casman SJ, Malyankar UM;
PI Tchernev VT, Vernet CAM, Spytek KA, Shenoy SG, Alsobrook JP;
PI Edinger S, Peyman JA, Stone DJ, Ellerman K, Gangolli EA, Boldog FL;
PI Colman SD, Eisen AJ, Liu X, Padigaru M, Spaderna SK, Zerhusen BD;
XX
DR WPI; 2002-547774/58.
DR N-PSDB; ABT05471.
XX
PT Novel isolated polypeptide, designated NOVX, useful for treating or
PT preventing cancer, diabetes, obesity, dyslipidemia, anorexia, and
PT metabolic, neurodegenerative, immune and hematopoietic disorders.
XX
PS Claim 1; Page 141; 421pp; English.
XX
CC The invention relates to an isolated polypeptide, designated NOVX,
CC comprising a sequence fully defined in the specification. The isolated
CC protein, its encoding polynucleotide or an antibody created from the
CC protein is useful in the manufacture of a medicament for treating a
CC syndrome associated with a human disease, preferably a NOVX-associated
CC disorder, or for treating or preventing a NOVX-associated disorder in a
CC subject, preferably human. The isolated protein, its encoding
CC polynucleotide or an antibody created from the protein are also useful
CC for treating or preventing metabolic disorders, diabetes, obesity,
CC infectious disease, anorexia, neurodegenerative disorder, Alzheimer's
CC disease, Parkinson's disorder, immune disorders, haematopoietic
CC disorders, and various dyslipidaemias, metabolic disturbances associated
CC with obesity, the metabolic syndrome X, wasting disorders associated with
CC chronic diseases, and cancer. The isolated protein, its encoding
CC polynucleotide or an antibody created from the protein are useful for
CC treating or preventing neurological disorders such as epilepsy, stroke,
CC mental disorders including mood, anxiety, schizophrenic disorders,
CC disorders of vesicular transport such as cystic fibrosis, diabetes
CC mellitus, goiter, gastrointestinal disorders including ulcerative
CC colitis, other conditions associated with abnormal vesicle trafficking
CC including AIDS, allergic reactions, multiple sclerosis and rheumatoid
CC arthritis. A cell comprising the vector of the invention is useful for
CC producing non-human transgenic animals. The polynucleotide of the
CC invention can be used to treat disorders by gene therapy. This sequence
CC represents one of the isolated NOVX proteins of the invention
XX
SQ Sequence 446 AA;

Query Match 89.5%; Score 2116; DB 5; Length 446;
Best Local Similarity 91.0%; Pred. No. 4.6e-192;
Matches 415; Conservative 1; Mismatches 2; Indels 38; Gaps 1;

```
Qy          1 MRKISNHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRATATQAFFSITRAAPGARWGQQAH 60
              ||||||||||||                                        ||||||||
Db         29 MRKISNHGSLRVAV------------------------------------ARWGQQAH 50

Qy         61 SPLGTAADGHEVFYGIMFDAGSTGTRVHVFQFTRPPRETPTLTHETFKAVKPGLSAYADD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||:||||||||||
Db         51 SPLGTAADGHEVFYGIMFDAGSTGTRVHVFQFTRPPRETPTLTHETFKALKPGLSAYADD 110

Qy        121 VEKSAQGIRELLDVAKQDIPFDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASP 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        111 VEKSAQGIRELLDVAKQDIPFDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKGVFKASP 170

Qy        181 FLVGDDCVSIMNGTDEGVSAWITINFLTGSLKTPGGSSVGMLDLGGGSTQIAFLPRVEGT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        171 FLVGDDCVSIMNGTDEGVSAWITINFLTGSLKTPGGSSVGMLDLGGGSTQIAFLPRVEGT 230

Qy        241 LQASPPGYLTALRMFNRTYKLYSYSYLGLGLMSARLAILGGVEGQPAKDGKELVSPCLSP 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        231 LQASPPGYLTALRMFNRTYKLYSYSYLGLGLMSARLAILGGVEGQPAKDGKELVSPCLSP 290

Qy        301 SFKGEWEHAEVTYRVSGQKAAASLHELCAARVSEVLQNRVHRTEEVKHVDFYAFSYYYDL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        291 SFKGEWEHAEVTYRVSGQKAAASLHELCAARVSEVLQNRVHRTEEVKHVDFYAFSYYYDL 350

Qy        361 AAGVGLIDAEKGGSLVVGDFEIAAKYVCRTLETQPQSSPFSCMDLTYVSLLLQEFGFPRS 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        351 AAGVGLIDAEKGGSLVVGDFEIAAKYVCRTLETQPQSSPFSCMDLTYVSLLLQEFGFPRS 410

Qy        421 KVLKLTRKIDNVETSWALGAIFHYIDSLNRQKSPAS 456
              |||||||||||||||||||||||||||||||||||
Db        411 KVLKLTRKIDNVETSWALGAIFHYIDSLNRQKSPAS 446
```

RESULT 12
AAB72242
ID AAB72242 standard; protein; 471 AA.
XX
AC AAB72242;
XX
DT 14-MAY-2001 (first entry)
XX
DE Mature human CD39 like protein CD39-L2 amino acid sequence.
XX
KW Human CD39-like protein; apyrase; NDPase; platelet function inhibitor;
KW myocardial infarction; cerebral ischaemia; angina; arterial thrombosis;
KW cerebral artery thrombosis; platelet aggregation; inflammation;
KW apoptosis; autoimmune disorder; neurological disorder;
KW Alzheimer's disease; Parkinson's disease; cancer; CD39-L2.
XX
OS Homo sapiens.
XX
PN WO200110205-A1.
XX
PD 15-FEB-2001.
XX
PF 09-AUG-2000; 2000WO-US021790.
XX
PR 09-AUG-1999; 99US-00370265.
PR 11-JAN-2000; 2000US-00481238.
PR 25-APR-2000; 2000US-00557800.
PR 26-MAY-2000; 2000US-00583231.
PR 30-JUN-2000; 2000US-00608285.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Ford J, Mulero JJ, Yeung G;
XX
DR WPI; 2001-147489/15.
DR N-PSDB; AAF63387.
XX
PT Polynucleotides encoding human CD39-like polypeptides, with apyrase
PT and/or NDPase activity, which are useful in the treatment of pathological
PT conditions caused by thrombosis (e.g. myocardial infarction) and
PT inflammatory disorders.
XX
PS Claim 53; Page 192-194; 203pp; English.
XX
CC This invention relates to polynucleotides encoding human CD39-like
CC polypeptides with apyrase and/or NDPase activity. The polypeptides having
CC ATPDase, including NDPase, activity are useful for inhibiting platelet
CC function and can therefore be used in the prophylaxis or treatment of
CC pathological conditions caused by or involving thrombosis or excessive
CC coagulation or excessive platelet aggregation, such as myocardial
CC infarction, cerebral ischaemia, angina, arterial thrombosis, cerebral
CC artery thrombosis or intracardiac thrombosis, and conditions associated
CC with venous thrombosis. CD39-L4 and CD39-L2 polypeptides are useful in
CC modulating disease states (including platelet aggregation, inflammation
CC and apoptosis) associated with ADP or other purinergic signalling by
CC reducing the levels of NDPs. The polypeptides are also useful for
CC prophylaxis or treatment of inflammation related disorders, such as
CC disorders involving sepsis or systemic inflammatory response syndrome or
CC SIRS (and associated conditions such as fever, tachycardia, tachypnea,

```
CC   cytokine overstimulation); autoimmune disorders such as thrombosis,
CC   atherosclerosis, acute pancreatitis, dermatitis, including psoriasis,
CC   cirrhosis, reperfusion injury, asthma, multiple sclerosis, arthritis;
CC   neurological disorders including neurodegenerative diseases, epilepsy,
CC   depression, Alzheimer's disease, Parkinson's disease, Huntington's
CC   disease, and amyotrophic lateral sclerosis; and cancer. The present
CC   sequence represents mature D39 like protein CD39-L2
XX
SQ   Sequence 471 AA;

  Query Match             84.7%;  Score 2003;  DB 4;  Length 471;
  Best Local Similarity   98.5%;  Pred. No. 2.8e-181;
  Matches  388;  Conservative    1;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 MRKISNHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRATATQAFFSITRAAPGARWGQQAH 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         29 MRKISNHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRATATQAFFSITRAAPGARWGQQAH 88

Qy         61 SPLGTAADGHEVFYGIMFDAGSTGTRVHVFQFTRPPRETPTLTHETFKAVKPGLSAYADD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         89 SPLGTAADGHEVFYGIMFDAGSTGTRVHVFQFTRPPRETPTLTHETFKAVKPGLSAYADD 148

Qy        121 VEKSAQGIRELLDVAKQDIPFDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASP 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        149 VEKSAQGIRELLDVAKQDIPFDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASP 208

Qy        181 FLVGDDCVSIMNGTDEGVSAWITINFLTGSLKTPGGSSVGMLDLGGGSTQIAFLPRVEGT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        209 FLVGDDCVSIMNGTDEGVSAWITINFLTGSLKTPGGSSVGMLDLGGGSTQIAFLPRVEGT 268

Qy        241 LQASPPGYLTALRMFNRTYKLYSYSYLGLGLMSARLAILGGVEGQPAKDGKELVSPCLSP 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        269 LQASPPGYLTALRMFNRTYKLYSYSYLGLGLMSARLAILGGVEGQPAKDGKELVSPCLSP 328

Qy        301 SFKGEWEHAEVTYRVSGQKAAASLHELCAARVSEVLQNRVHRTEEVKHVDFYAFSYYYDL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        329 SFKGEWEHAEVTYRVSGQKAAASLHELCAARVSEVLQNRVHRTEEVKHVDFYAFSYYYDL 388

Qy        361 AAGVGLIDAEKGGSLVVGDFEIAAKYVCRTLETQ 394
              |||||||||||||||||||||||||     || :
Db        389 AAGVGLIDAEKGGSLVVGDFEIAAKYGGSHLERE 422


RESULT 13
AAY44849
ID   AAY44849 standard; protein; 428 AA.
XX
AC   AAY44849;
XX
DT   18-MAY-2000  (first entry)
XX
DE   Human CD39-L4 protein.
XX
KW   CD39-L4; human; apyrase; nucleotide diphosphatase; NDPase;
KW   ATP Diphosphohydrolase; ATPDase; adenosine diphosphate; ADP; treatment;
KW   platelet aggregation; antithrombotic; thrombosis; myocardial infarction;
KW   cerebral ischaemia; angina; vascular graft; extracorporeal circulation;
KW   molecular weight marker; nutritional supplement; tumour; prevention;
KW   drug targeting; Apyrase Conserved Region; ACR.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide          1. .22
FT                    /label= Leader_peptide
FT   Protein          23. .428
FT                    /label= Mature_human_CD39-L4_protein
FT                    /note= "Homologous to human and murine CD39"
FT   Binding-site     54. .58
FT                    /label= ATP_Binding_region
FT   Region           129. .134
FT                    /label= Apyrase_Conserved_Region
FT   Region           169. .173
FT                    /label= Apyrase_Conserved_Region
FT   Region           199. .206
FT                    /note= "Conserved motif in ATPDases"
XX
PN   WO200004041-A2.
XX
PD   27-JAN-2000.
XX
PF   16-JUL-1999;   99WO-US016180.
XX
PR   16-JUL-1998;   98US-00118205.
PR   24-JUL-1998;   98US-00122449.
PR   04-FEB-1999;   99US-00244444.
PR   19-MAR-1999;   99US-00273447.
PR   09-JUL-1999;   99US-00350836.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Ford J,  Mulero J;
XX
DR   WPI; 2000-182397/16.
DR   N-PSDB; AAZ50356, AAZ50359.
XX
PT   New nucleic acid encoding human CD39-like protein, useful for treating
PT   and preventing thrombotic disease.
XX
PS   Claim 15; Fig 2; 125pp; English.
XX
CC   The present amino acid sequence is the CD39-L4 protein, an apyrase and/or
CC   nucleotide diphosphatase (NDPase). It is isolated from the human foetal
CC   liver-spleen cDNA library, b2HFLS20W. It is a soluble ATP
CC   Diphosphohydrolases (ATPDase) and is involved in the hydrolysis of
CC   adenosine diphosphate (ADP), the agonist that causes platelet
CC   aggregation. CD39-L4 protein has 30% and 80% homology to human and murine
CC   CD39. It has platelet aggregation inhibition and antithrombotic activity.
CC   CD39-L4 is used to treat or prevent thrombosis, myocardial infarction,
CC   cerebral ischaemia and angina. It is also used in vitro, to maintain
CC   vascular grafts or during extracorporeal circulation, to hydrolyse NDP,
CC   as molecular weight markers and as nutritional supplements. It is used to
CC   identify therapeutic agents that bind and modulate CD39-L4. It is coupled
CC   to toxins for targeting drugs to tumours or other cells that express CD39
CC   -L4
XX
SQ   Sequence 428 AA;

  Query Match             42.3%;  Score 999;  DB 3;  Length 428;
  Best Local Similarity   52.4%;  Pred. No. 8.6e-86;
  Matches  204;  Conservative   56;  Mismatches  123;  Indels    6;  Gaps    4;

Qy         62 PLGTAADGHEVFYGIMFDAGSTGTRVHVFQFT-RPPRETPTLTHETFKAVKPGLSAYADD 120
              |:  :|      |||||||||||||:||: |  : | : | |   | | :|||||||: |
Db         40 PINVSA---STLYGIMFDAGSTGTRIHVYTFVQKMPGQLPILEGEVFDSVKPGLSAFVDQ 96

Qy        121 VEKSAQGIRELLDVAKQDIPFDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASP 180
               :: |: :: ||:|||  ||   || ||:|||||||||||||  ||: || :|||:|: ||
Db         97 PKQGAETVQGLLEVAKDSIPRSHWKKTPVVLKATAGLRLLPEHKAKALLFEVKEIFRKSP 156

Qy        181 FLVGDDCVSIMNGTDEGVSAWITINFLTGSLKTPGGSSVGMLDLGGGSTQIAFLPRVEGT 240
              |||    ||||:|:|||: ||:|:|||||  |      :|: ||||| |||| |||: | |
Db        157 FLVPKGSVSIMDGSDEGILAWVTVNFLTGQLHGHRQETVGTLDLGGASTQITFLPQFEKT 216

Qy        241 LQASPPGYLTALRMFNRTYKLYSYSYLGLGLMSARLAILGGVEGQPAKDGKELVSPCLSP 300
              |: :| ||||:  ||| |||||::|||| || :|||| || :| :   ||    | ||
Db        217 LEQTPRGYLTSFEMFNSTYKLYTHSYLGFGLKAARLATLGALETE-GTDGHTFRSACLPR 275

Qy        301 SFKGEWEHAEVTYRVSGQKAAASLHELCAARVSEVLQNRVHRTEEVKHVDFYAFSYYYDL 360
              : ||    | |:  | :      | | | |  |:: ::|: |||:   |||||||||
Db        276 WLEAEWIFGGVKYQYGGNQEGEVGFEPCYAEVLRVVRGKLHQPEEVQRGSFYAFSYYYDR 335

Qy        361 AAGVGLIDAEKGGSLVVGDFEIAAKYVCRTLETQPQSSPFSCMDLTYVSLLLQE-FGFPR 419
              |    :|| |||| | | |||  |: ||  ||     ||| ||||:|:: ||:: |||
Db        336 AVDTDMIDYEKGGILKVEDFERKAREVCDNLENFTSGSPFLCMDLSYITALLKDGFGFAD 395
```

```
Qy        420 SKVLKLTRKIDNVETSWALGAIFHYIDSL 448
              | ||:||:|::|:|| ||||| || : ||
Db        396 STVLQLTKKVNNIETGWALGATFHLLQSL 424
```

RESULT 14
AAB72238
ID AAB72238 standard; protein; 428 AA.
XX
AC AAB72238;
XX
DT 14-MAY-2001 (first entry)
XX
DE Human CD39 like protein CD39-L4 amino acid sequence.
XX
KW Human CD39-like protein; apyrase; NDPase; platelet function inhibitor;
KW myocardial infarction; cerebral ischaemia; angina; arterial thrombosis;
KW cerebral artery thrombosis; platelet aggregation; inflammation;
KW apoptosis; autoimmune disorder; neurological disorder;
KW Alzheimer's disease; Parkinson's disease; cancer; CD39-L4.
XX
OS Homo sapiens.
XX
PN WO200110205-A1.
XX
PD 15-FEB-2001.
XX
PF 09-AUG-2000; 2000WO-US021790.
XX
PR 09-AUG-1999; 99US-00370265.
PR 11-JAN-2000; 2000US-00481238.
PR 25-APR-2000; 2000US-00557800.
PR 26-MAY-2000; 2000US-00583231.
PR 30-JUN-2000; 2000US-00608285.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Ford J, Mulero JJ, Yeung G;
XX
DR WPI; 2001-147489/15.
DR N-PSDB; AAF63383.
XX
PT Polynucleotides encoding human CD39-like polypeptides, with apyrase
PT and/or NDPase activity, which are useful in the treatment of pathological
PT conditions caused by thrombosis (e.g. myocardial infarction) and
PT inflammatory disorders.
XX
PS Claim 15; Fig 2; 203pp; English.
XX
CC This invention relates to polynucleotides encoding human CD39-like
CC polypeptides with apyrase and/or NDPase activity. The polypeptides having
CC ATPDase, including NDPase, activity are useful for inhibiting platelet
CC function and can therefore be used in the prophylaxis or treatment of
CC pathological conditions caused by or involving thrombosis or excessive
CC coagulation or excessive platelet aggregation, such as myocardial
CC infarction, cerebral ischaemia, angina, arterial thrombosis, cerebral
CC artery thrombosis or intracardiac thrombosis, and conditions associated
CC with venous thrombosis. CD39-L4 and CD39-L2 polypeptides are useful in
CC modulating disease states (including platelet aggregation, inflammation
CC and apoptosis) associated with ADP or other purinergic signalling by
CC reducing the levels of NDPs. The polypeptides are also useful for
CC prophylaxis or treatment of inflammation related disorders, such as
CC disorders involving sepsis or systemic inflammatory response syndrome or
CC SIRS (and associated conditions such as fever, tachycardia, tachypnea,
CC cytokine overstimulation); autoimmune disorders such as thrombosis,
CC atherosclerosis, acute pancreatitis, dermatitis, including psoriasis,
CC cirrhosis, reperfusion injury, asthma, multiple sclerosis, arthritis;
CC neurological disorders including neurodegenerative diseases, epilepsy,
CC depression, Alzheimer's disease, Parkinson's disease, Huntington's
CC disease, and amyotrophic lateral sclerosis; and cancer. The present
CC sequence represents human CD39 like protein CD39-L4
XX
SQ Sequence 428 AA;

Query Match 42.3%; Score 999; DB 4; Length 428;
Best Local Similarity 52.4%; Pred. No. 8.6e-86;
Matches 204; Conservative 56; Mismatches 123; Indels 6; Gaps 4;

```
Qy         62 PLGTAADGHEVFYGIMFDAGSTGTRVHVFQFT-RPPRETPTLTHETFKAVKPGLSAYADD 120
              |:  :|       |||||||||||||:||: |  : | : | |  | | :|||||||: |
Db         40 PINVSA---STLYGIMFDAGSTGTRIHVYTFVQKMPGQLPILEGEVFDSVKPGLSAFVDQ 96

Qy        121 VEKSAQGIRELLDVAKQDIPFDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASP 180
               :: |: :: ||:|||  ||   || ||:|||||||||||  ||: || :|||:|: ||
Db         97 PKQGAETVQGLLEVAKDSIPRSHWKKTPVVLKATAGLRLLPEHKAKALLFEVKEIFRKSP 156

Qy        181 FLVGDDCVSIMNGTDEGVSAWITINFLTGSLKTPGGSSVGMLDLGGGSTQIAFLPRVEGT 240
              |||    ||||:|:|||: ||:|:|||||  |      :|| ||||| |||| |||: | |
Db        157 FLVPKGSVSIMDGSDEGILAWVTVNFLTGQLHGHRQETVGTLDLGGASTQITFLPQFEKT 216

Qy        241 LQASPPGYLTALRMFNRTYKLYSYSYLGLGLMSARLAILGGVEGQPAKDGKELVSPCLSP 300
              |: :| ||||:  ||| ||||::|||| || :|||| || :| :   ||    | ||
Db        217 LEQTPRGYLTSFEMFNSTYKLYTHSYLGFGLKAARLATLGALETE-GTDGHTFRSACLPR 275

Qy        301 SFKGEWEHAEVTYRVSGQKAAASLHELCAARVSEVLQNRVHRTEEVKHVDFYAFSYYYDL 360
              : ||    | |:  | :       | | | |  |:: ::|: |||:   ||||||||
Db        276 WLEAEWIFGGVKYQYGGNQEGEVGFEPCYAEVLRVVRGKLHQPEEVQRGSFYAFSYYYDR 335

Qy        361 AAGVGLIDAEKGGSLVVGDFEIAAKYVCRTLETQPQSSPFSCMDLTYVSLLLQE-FGFPR 419
              |    :|| |||| | | |||  |: ||  ||     ||| ||||:|:: ||:: |||
Db        336 AVDTDMIDYEKGGILKVEDFERKAREVCDNLENFTSGSPFLCMDLSYITALLKDGFGFAD 395

Qy        420 SKVLKLTRKIDNVETSWALGAIFHYIDSL 448
              | ||:||:|::|:|| ||||| || : ||
Db        396 STVLQLTKKVNNIETGWALGATFHLLQSL 424
```

RESULT 15
AAB72243
ID AAB72243 standard; protein; 428 AA.
XX
AC AAB72243;
XX
DT 14-MAY-2001 (first entry)
XX
DE Human CD39 like protein CD39-L4 amino acid sequence.
XX
KW Human CD39-like protein; apyrase; NDPase; platelet function inhibitor;
KW myocardial infarction; cerebral ischaemia; angina; arterial thrombosis;
KW cerebral artery thrombosis; platelet aggregation; inflammation;
KW apoptosis; autoimmune disorder; neurological disorder;
KW Alzheimer's disease; Parkinson's disease; cancer; CD39-L4.
XX
OS Homo sapiens.
XX
PN WO200110205-A1.
XX
PD 15-FEB-2001.
XX
PF 09-AUG-2000; 2000WO-US021790.
XX
PR 09-AUG-1999; 99US-00370265.
PR 11-JAN-2000; 2000US-00481238.
PR 25-APR-2000; 2000US-00557800.
PR 26-MAY-2000; 2000US-00583231.
PR 30-JUN-2000; 2000US-00608285.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Ford J, Mulero JJ, Yeung G;
XX
DR WPI; 2001-147489/15.
DR N-PSDB; AAF63402.
XX
PT Polynucleotides encoding human CD39-like polypeptides, with apyrase
PT and/or NDPase activity, which are useful in the treatment of pathological

PT conditions caused by thrombosis (e.g. myocardial infarction) and
PT inflammatory disorders.
XX
PS Example 9; Page 142-144; 203pp; English.
XX
CC This invention relates to polynucleotides encoding human CD39-like
CC polypeptides with apyrase and/or NDPase activity. The polypeptides having
CC ATPDase, including NDPase, activity are useful for inhibiting platelet
CC function and can therefore be used in the prophylaxis or treatment of
CC pathological conditions caused by or involving thrombosis or excessive
CC coagulation or excessive platelet aggregation, such as myocardial
CC infarction, cerebral ischaemia, angina, arterial thrombosis, cerebral
CC artery thrombosis or intracardiac thrombosis, and conditions associated
CC with venous thrombosis. CD39-L4 and CD39-L2 polypeptides are useful in
CC modulating disease states (including platelet aggregation, inflammation
CC and apoptosis) associated with ADP or other purinergic signalling by
CC reducing the levels of NDPs. The polypeptides are also useful for
CC prophylaxis or treatment of inflammation related disorders, such as
CC disorders involving sepsis or systemic inflammatory response syndrome or
CC SIRS (and associated conditions such as fever, tachycardia, tachypnea,
CC cytokine overstimulation); autoimmune disorders such as thrombosis,
CC atherosclerosis, acute pancreatitis, dermatitis, including psoriasis,
CC cirrhosis, reperfusion injury, asthma, multiple sclerosis, arthritis;
CC neurological disorders including neurodegenerative diseases, epilepsy,
CC depression, Alzheimer's disease, Parkinson's disease, Huntington's
CC disease, and amyotrophic lateral sclerosis; and cancer. The present
CC sequence represents the CD39 like protein CD39-L4 amino acid sequence
XX
SQ Sequence 428 AA;

Query Match 42.3%; Score 999; DB 4; Length 428;
Best Local Similarity 52.4%; Pred. No. 8.6e-86;
Matches 204; Conservative 56; Mismatches 123; Indels 6; Gaps 4;

```
Qy         62 PLGTAADGHEVFYGIMFDAGSTGTRVHVFQFT-RPPRETPTLTHETFKAVKPGLSAYADD 120
              |:  :|       |||||||||||||:||: |  : | : | |  | | :|||||||: |
Db         40 PINVSA---STLYGIMFDAGSTGTRIHVYTFVQKMPGQLPILEGEVFDSVKPGLSAFVDQ 96

Qy        121 VEKSAQGIRELLDVAKQDIPFDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASP 180
               :: |: :: ||:|||  ||   || ||:|||||||||||  ||: || :|||:|: ||
Db         97 PKQGAETVQGLLEVAKDSIPRSHWKKTPVVLKATAGLRLLPEHKAKALLFEVKEIFRKSP 156

Qy        181 FLVGDDCVSIMNGTDEGVSAWITINFLTGSLKTPGGSSVGMLDLGGGSTQIAFLPRVEGT 240
              |||    ||||:|:|||: ||:|:|||||  |      :|| ||||| |||| |||: | |
Db        157 FLVPKGSVSIMDGSDEGILAWVTVNFLTGQLHGHRQETVGTLDLGGASTQITFLPQFEKT 216

Qy        241 LQASPPGYLTALRMFNRTYKLYSYSYLGLGLMSARLAILGGVEGQPAKDGKELVSPCLSP 300
              |: :| ||||:  ||| |||||::|||| || :|||| || :| :   ||    | ||
Db        217 LEQTPRGYLTSFEMFNSTYKLYTHSYLGFGLKAARLATLGALETE-GTDGHTFRSACLPR 275

Qy        301 SFKGEWEHAEVTYRVSGQKAAASLHELCAARVSEVLQNRVHRTEEVKHVDFYAFSYYYDL 360
               : ||    | |:  | :       | | | |  |:: ::|: |||:   |||||||||
Db        276 WLEAEWIFGGVKYQYGGNQEGEVGFEPCYAEVLRVVRGKLHQPEEVQRGSFYAFSYYYDR 335

Qy        361 AAGVGLIDAEKGGSLVVGDFEIAAKYVCRTLETQPQSSPFSCMDLTYVSLLLQE-FGFPR 419
              |    :|| |||| | | |||  |: ||  ||    ||| ||||:|:: ||:: |||
Db        336 AVDTDMIDYEKGGILKVEDFERKAREVCDNLENFTSGSPFLCMDLSYITALLKDGFGFAD 395

Qy        420 SKVLKLTRKIDNVETSWALGAIFHYIDSL 448
              | ||:||:|::|:|| ||||| || : ||
Db        396 STVLQLTKKVNNIETGWALGATFHLLQSL 424
```

Search completed: November 16, 2004, 16:56:11
Job time : 160 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: November 16, 2004, 16:59:49 ; Search time 142 Seconds
(without alignments)
1136.208 Million cell updates/sec

Title: US-09-905-589A-2
Perfect score: 2364
Sequence: 1 MRKISNHGSLRVAKVAYPLG.....ALGAIFHYIDSLNRQKSPAS 456

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1568699 seqs, 353819137 residues

Total number of hits satisfying chosen parameters: 1568699

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep:*
17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2364	100.0	484	13	US-10-092-063-27	Sequence 27, Appl
2	2364	100.0	484	14	US-10-286-926-27	Sequence 27, Appl
3	2364	100.0	484	15	US-10-231-913-123	Sequence 123, App
4	2361	99.9	467	15	US-10-231-913-36	Sequence 36, Appl
5	2357	99.7	484	15	US-10-231-913-124	Sequence 124, App
6	2116	89.5	446	15	US-10-231-913-38	Sequence 38, Appl
7	2063.5	87.3	455	15	US-10-231-913-125	Sequence 125, App
8	1954	82.7	379	15	US-10-231-913-271	Sequence 271, App
9	1007	42.6	427	15	US-10-231-913-126	Sequence 126, App
10	999	42.3	428	13	US-10-091-085-3	Sequence 3, Appli
11	999	42.3	428	13	US-10-091-085-5	Sequence 5, Appli
12	999	42.3	428	13	US-10-092-063-3	Sequence 3, Appli
13	999	42.3	428	13	US-10-092-063-5	Sequence 5, Appli
14	999	42.3	428	14	US-10-286-926-3	Sequence 3, Appli
15	999	42.3	428	14	US-10-286-926-5	Sequence 5, Appli
16	999	42.3	428	15	US-10-231-913-127	Sequence 127, App
17	996	42.1	428	13	US-10-091-085-7	Sequence 7, Appli
18	996	42.1	428	13	US-10-092-063-7	Sequence 7, Appli
19	996	42.1	428	14	US-10-286-926-7	Sequence 7, Appli
20	992	42.0	428	16	US-10-408-765A-2296	Sequence 2296, Ap
21	909	38.5	405	13	US-10-092-063-25	Sequence 25, Appl
22	909	38.5	405	14	US-10-286-926-25	Sequence 25, Appl
23	909	38.5	465	13	US-10-092-063-39	Sequence 39, Appl
24	823	34.8	330	9	US-09-925-299-876	Sequence 876, App
25	823	34.8	330	10	US-09-925-299-876	Sequence 876, App
26	590.5	25.0	479	14	US-10-369-493-6447	Sequence 6447, Ap
27	525.5	22.2	467	9	US-09-129-112-19	Sequence 19, Appl
28	508.5	21.5	433	15	US-10-425-114-36762	Sequence 36762, A
29	508	21.5	556	14	US-10-369-493-2169	Sequence 2169, Ap
30	506	21.4	462	9	US-09-129-112-2	Sequence 2, Appli
31	504	21.3	467	15	US-10-425-114-45875	Sequence 45875, A
32	501	21.2	459	9	US-09-129-112-9	Sequence 9, Appli
33	500.5	21.2	562	17	US-10-425-115-334052	Sequence 334052,
34	500	21.2	467	15	US-10-424-599-230158	Sequence 230158,
35	498	21.1	518	14	US-10-369-493-1713	Sequence 1713, Ap
36	491	20.8	534	16	US-10-437-963-132351	Sequence 132351,
37	490.5	20.7	443	15	US-10-425-114-49933	Sequence 49933, A
38	489	20.7	464	17	US-10-425-115-185050	Sequence 185050,
39	483	20.4	457	15	US-10-425-114-51762	Sequence 51762, A
40	483	20.4	459	15	US-10-424-599-145076	Sequence 145076,
41	478.5	20.2	410	15	US-10-231-913-272	Sequence 272, App
42	467	19.8	469	17	US-10-739-930-10227	Sequence 10227, A
43	463	19.6	462	9	US-09-129-112-15	Sequence 15, Appl
44	452.5	19.1	516	17	US-10-425-115-338300	Sequence 338300,
45	447	18.9	463	17	US-10-425-115-213115	Sequence 213115,

ALIGNMENTS

```
RESULT 1
US-10-092-063-27
; Sequence 27, Application US/10092063
; Publication No. US20020173005A1
; GENERAL INFORMATION:
;  APPLICANT: Ford, John
;  APPLICANT:  Mulero, Julio
;  TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE POLYPEPTIDES
;  FILE REFERENCE: 28110/35908
;  CURRENT APPLICATION NUMBER: US/10/092,063
;  CURRENT FILING DATE:  2002-03-05
;  PRIOR APPLICATION NUMBER: 09/370,265
;  PRIOR FILING DATE: 2002-01-31
;  PRIOR APPLICATION NUMBER: PCT/US99/16180
;  PRIOR FILING DATE: 1999-07-16
;  PRIOR APPLICATION NUMBER: 09/350,836
;  PRIOR FILING DATE: 1999-07-09
;  PRIOR APPLICATION NUMBER: 09/273,447
;  PRIOR FILING DATE: 1999-03-19
;  PRIOR APPLICATION NUMBER: 09/244,444
;  PRIOR FILING DATE: 1999-02-04
;  PRIOR APPLICATION NUMBER: 09/122,449
;  PRIOR FILING DATE: 1998-07-24
;  PRIOR APPLICATION NUMBER: 09/118,205
;  PRIOR FILING DATE: 1998-07-16
;  NUMBER OF SEQ ID NOS: 39
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 27
;   LENGTH: 484
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-092-063-27

  Query Match            100.0%;  Score 2364;  DB 13;  Length 484;
  Best Local Similarity  100.0%;  Pred. No. 8.7e-218;
  Matches  456;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy          1 MRKISNHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRATATQAFFSITRAAPGARWGQQAH 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         29 MRKISNHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRATATQAFFSITRAAPGARWGQQAH 88

Qy         61 SPLGTAADGHEVFYGIMFDAGSTGTRVHVFQFTRPPRETPTLTHETFKAVKPGLSAYADD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         89 SPLGTAADGHEVFYGIMFDAGSTGTRVHVFQFTRPPRETPTLTHETFKAVKPGLSAYADD 148

Qy        121 VEKSAQGIRELLDVAKQDIPFDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASP 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        149 VEKSAQGIRELLDVAKQDIPFDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASP 208

Qy        181 FLVGDDCVSIMNGTDEGVSAWITINFLTGSLKTPGGSSVGMLDLGGGSTQIAFLPRVEGT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        209 FLVGDDCVSIMNGTDEGVSAWITINFLTGSLKTPGGSSVGMLDLGGGSTQIAFLPRVEGT 268

Qy        241 LQASPPGYLTALRMFNRTYKLYSYSYLGLGLMSARLAILGGVEGQPAKDGKELVSPCLSP 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        269 LQASPPGYLTALRMFNRTYKLYSYSYLGLGLMSARLAILGGVEGQPAKDGKELVSPCLSP 328

Qy        301 SFKGEWEHAEVTYRVSGQKAAASLHELCAARVSEVLQNRVHRTEEVKHVDFYAFSYYYDL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        329 SFKGEWEHAEVTYRVSGQKAAASLHELCAARVSEVLQNRVHRTEEVKHVDFYAFSYYYDL 388

Qy        361 AAGVGLIDAEKGGSLVVGDFEIAAKYVCRTLETQPQSSPFSCMDLTYVSLLLQEFGFPRS 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        389 AAGVGLIDAEKGGSLVVGDFEIAAKYVCRTLETQPQSSPFSCMDLTYVSLLLQEFGFPRS 448

Qy        421 KVLKLTRKIDNVETSWALGAIFHYIDSLNRQKSPAS 456
              ||||||||||||||||||||||||||||||||||||
Db        449 KVLKLTRKIDNVETSWALGAIFHYIDSLNRQKSPAS 484
```

RESULT 2
US-10-286-926-27
; Sequence 27, Application US/10286926
; Publication No. US20030175752A1
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; APPLICANT: Yeung, George
; TITLE OF INVENTION: Methods and Materials Relating to CD39-Like
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 28110/36457CON
; CURRENT APPLICATION NUMBER: US/10/286,926
; CURRENT FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: 09/557,800
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/481,238
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 09/370,265
; PRIOR FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: PCT/US99/16180
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/350836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273447
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/122449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/244444
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 27
; LENGTH: 484
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-286-926-27

Query Match 100.0%; Score 2364; DB 14; Length 484;
Best Local Similarity 100.0%; Pred. No. 8.7e-218;
Matches 456; Conservative 0; Mismatches 0; Indels 0; Gaps 0;


```
Qy          1 MRKISNHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRATATQAFFSITRAAPGARWGQQAH 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         29 MRKISNHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRATATQAFFSITRAAPGARWGQQAH 88

Qy         61 SPLGTAADGHEVFYGIMFDAGSTGTRVHVFQFTRPPRETPTLTHETFKAVKPGLSAYADD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         89 SPLGTAADGHEVFYGIMFDAGSTGTRVHVFQFTRPPRETPTLTHETFKAVKPGLSAYADD 148

Qy        121 VEKSAQGIRELLDVAKQDIPFDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASP 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        149 VEKSAQGIRELLDVAKQDIPFDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASP 208

Qy        181 FLVGDDCVSIMNGTDEGVSAWITINFLTGSLKTPGGSSVGMLDLGGGSTQIAFLPRVEGT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        209 FLVGDDCVSIMNGTDEGVSAWITINFLTGSLKTPGGSSVGMLDLGGGSTQIAFLPRVEGT 268

Qy        241 LQASPPGYLTALRMFNRTYKLYSYSYLGLGLMSARLAILGGVEGQPAKDGKELVSPCLSP 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        269 LQASPPGYLTALRMFNRTYKLYSYSYLGLGLMSARLAILGGVEGQPAKDGKELVSPCLSP 328

Qy        301 SFKGEWEHAEVTYRVSGQKAAASLHELCAARVSEVLQNRVHRTEEVKHVDFYAFSYYYDL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        329 SFKGEWEHAEVTYRVSGQKAAASLHELCAARVSEVLQNRVHRTEEVKHVDFYAFSYYYDL 388

Qy        361 AAGVGLIDAEKGGSLVVGDFEIAAKYVCRTLETQPQSSPFSCMDLTYVSLLLQEFGFPRS 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        389 AAGVGLIDAEKGGSLVVGDFEIAAKYVCRTLETQPQSSPFSCMDLTYVSLLLQEFGFPRS 448

Qy        421 KVLKLTRKIDNVETSWALGAIFHYIDSLNRQKSPAS 456
              ||||||||||||||||||||||||||||||||||||
Db        449 KVLKLTRKIDNVETSWALGAIFHYIDSLNRQKSPAS 484
```


RESULT 3
US-10-231-913-123
; Sequence 123, Application US/10231913
; Publication No. US20040005576A1
; GENERAL INFORMATION:
; APPLICANT: Guo, Xiaojia S.
; APPLICANT: Li, Li
; APPLICANT: Patturajan, Meera
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Casman, Stacie J.
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Tchernev, Velizar T.
; APPLICANT: Vernet, Corine A.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Alsobrook II, John P.
; APPLICANT: Edinger, Schlomit
; APPLICANT: Peyman, John A.
; APPLICANT: Stone, David J.
; APPLICANT: Ellerman, Karen
; APPLICANT: Gangolli, Esha A.
; APPLICANT: Boldog, Ference L.
; APPLICANT: Colman, Steven D.
; APPLICANT: Eisen, Andrew J.
; APPLICANT: Liu, Xiaohong
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Spaderna, Steven K.
; APPLICANT: Zerhusen, Bryan D.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-216
; CURRENT APPLICATION NUMBER: US/10/231,913
; CURRENT FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: 60/251,660
; PRIOR FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: 60/255,029
; PRIOR FILING DATE: 2000-12-12

```
;  PRIOR APPLICATION NUMBER: 60/260,326
;  PRIOR FILING DATE: 2001-01-08
;  PRIOR APPLICATION NUMBER: 60/263,800
;  PRIOR FILING DATE: 2001-01-24
;  PRIOR APPLICATION NUMBER: 60/269,942
;  PRIOR FILING DATE: 2001-02-20
;  PRIOR APPLICATION NUMBER: 60/286,183
;  PRIOR FILING DATE: 2001-04-24
;  PRIOR APPLICATION NUMBER: 60/313,627
;  PRIOR FILING DATE: 2001-08-20
;  PRIOR APPLICATION NUMBER: 60/318,712
;  PRIOR FILING DATE: 2001-09-12
;  NUMBER OF SEQ ID NOS: 292
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 123
;   LENGTH: 484
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-231-913-123

  Query Match           100.0%;  Score 2364;  DB 15;  Length 484;
  Best Local Similarity  100.0%;  Pred. No. 8.7e-218;
  Matches  456;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRKISNHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRATATQAFFSITRAAPGARWGQQAH 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         29 MRKISNHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRATATQAFFSITRAAPGARWGQQAH 88

Qy         61 SPLGTAADGHEVFYGIMFDAGSTGTRVHVFQFTRPPRETPTLTHETFKAVKPGLSAYADD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         89 SPLGTAADGHEVFYGIMFDAGSTGTRVHVFQFTRPPRETPTLTHETFKAVKPGLSAYADD 148

Qy        121 VEKSAQGIRELLDVAKQDIPFDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASP 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        149 VEKSAQGIRELLDVAKQDIPFDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASP 208

Qy        181 FLVGDDCVSIMNGTDEGVSAWITINFLTGSLKTPGGSSVGMLDLGGGSTQIAFLPRVEGT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        209 FLVGDDCVSIMNGTDEGVSAWITINFLTGSLKTPGGSSVGMLDLGGGSTQIAFLPRVEGT 268

Qy        241 LQASPPGYLTALRMFNRTYKLYSYSYLGLGLMSARLAILGGVEGQPAKDGKELVSPCLSP 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        269 LQASPPGYLTALRMFNRTYKLYSYSYLGLGLMSARLAILGGVEGQPAKDGKELVSPCLSP 328

Qy        301 SFKGEWEHAEVTYRVSGQKAAASLHELCAARVSEVLQNRVHRTEEVKHVDFYAFSYYYDL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        329 SFKGEWEHAEVTYRVSGQKAAASLHELCAARVSEVLQNRVHRTEEVKHVDFYAFSYYYDL 388

Qy        361 AAGVGLIDAEKGGSLVVGDFEIAAKYVCRTLETQPQSSPFSCMDLTYVSLLLQEFGFPRS 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        389 AAGVGLIDAEKGGSLVVGDFEIAAKYVCRTLETQPQSSPFSCMDLTYVSLLLQEFGFPRS 448

Qy        421 KVLKLTRKIDNVETSWALGAIFHYIDSLNRQKSPAS 456
              ||||||||||||||||||||||||||||||||||||
Db        449 KVLKLTRKIDNVETSWALGAIFHYIDSLNRQKSPAS 484


RESULT 4
US-10-231-913-36
; Sequence 36, Application US/10231913
; Publication No. US20040005576A1
; GENERAL INFORMATION:
;  APPLICANT: Guo, Xiaojia S.
;  APPLICANT:  Li, Li
;  APPLICANT:  Patturajan, Meera
;  APPLICANT:  Shimkets, Richard A.
;  APPLICANT:  Casman, Stacie J.
;  APPLICANT:  Malyankar, Uriel M.
;  APPLICANT:  Tchernev, Velizar T.
;  APPLICANT:  Vernet, Corine A.
;  APPLICANT:  Spytek, Kimberly A.
;  APPLICANT:  Shenoy, Suresh G.
;  APPLICANT:  Alsobrook II, John P.
;  APPLICANT:  Edinger, Schlomit
;  APPLICANT:  Peyman, John A.
;  APPLICANT:  Stone, David J.
;  APPLICANT:  Ellerman, Karen
;  APPLICANT:  Gangolli, Esha A.
;  APPLICANT:  Boldog, Ference L.
;  APPLICANT:  Colman, Steven D.
;  APPLICANT:  Eisen, Andrew J.
;  APPLICANT:  Liu, Xiaohong
;  APPLICANT:  Padigaru, Muralidhara
;  APPLICANT:  Spaderna, Steven K.
;  APPLICANT:  Zerhusen, Bryan D.
;  TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
;  FILE REFERENCE: 21402-216
;  CURRENT APPLICATION NUMBER: US/10/231,913
;  CURRENT FILING DATE:  2002-08-30
;  PRIOR APPLICATION NUMBER: 60/251,660
;  PRIOR FILING DATE: 2000-12-06
;  PRIOR APPLICATION NUMBER: 60/255,029
;  PRIOR FILING DATE: 2000-12-12
;  PRIOR APPLICATION NUMBER: 60/260,326
;  PRIOR FILING DATE: 2001-01-08
;  PRIOR APPLICATION NUMBER: 60/263,800
;  PRIOR FILING DATE: 2001-01-24
;  PRIOR APPLICATION NUMBER: 60/269,942
;  PRIOR FILING DATE: 2001-02-20
;  PRIOR APPLICATION NUMBER: 60/286,183
;  PRIOR FILING DATE: 2001-04-24
;  PRIOR APPLICATION NUMBER: 60/313,627
;  PRIOR FILING DATE: 2001-08-20
;  PRIOR APPLICATION NUMBER: 60/318,712
;  PRIOR FILING DATE: 2001-09-12
;  NUMBER OF SEQ ID NOS: 292
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 36
;   LENGTH: 467
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-231-913-36

  Query Match           99.9%;  Score 2361;  DB 15;  Length 467;
  Best Local Similarity  99.8%;  Pred. No. 1.6e-217;
  Matches  455;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRKISNHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRATATQAFFSITRAAPGARWGQQAH 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         12 MRKISNHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRATATQAFFSITRAAPGARWGQQAH 71

Qy         61 SPLGTAADGHEVFYGIMFDAGSTGTRVHVFQFTRPPRETPTLTHETFKAVKPGLSAYADD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||:|||||||||||
Db         72 SPLGTAADGHEVFYGIMFDAGSTGTRVHVFQFTRPPRETPTLTHETFKALKPGLSAYADD 131

Qy        121 VEKSAQGIRELLDVAKQDIPFDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASP 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        132 VEKSAQGIRELLDVAKQDIPFDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASP 191

Qy        181 FLVGDDCVSIMNGTDEGVSAWITINFLTGSLKTPGGSSVGMLDLGGGSTQIAFLPRVEGT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        192 FLVGDDCVSIMNGTDEGVSAWITINFLTGSLKTPGGSSVGMLDLGGGSTQIAFLPRVEGT 251

Qy        241 LQASPPGYLTALRMFNRTYKLYSYSYLGLGLMSARLAILGGVEGQPAKDGKELVSPCLSP 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        252 LQASPPGYLTALRMFNRTYKLYSYSYLGLGLMSARLAILGGVEGQPAKDGKELVSPCLSP 311

Qy        301 SFKGEWEHAEVTYRVSGQKAAASLHELCAARVSEVLQNRVHRTEEVKHVDFYAFSYYYDL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        312 SFKGEWEHAEVTYRVSGQKAAASLHELCAARVSEVLQNRVHRTEEVKHVDFYAFSYYYDL 371

Qy        361 AAGVGLIDAEKGGSLVVGDFEIAAKYVCRTLETQPQSSPFSCMDLTYVSLLLQEFGFPRS 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        372 AAGVGLIDAEKGGSLVVGDFEIAAKYVCRTLETQPQSSPFSCMDLTYVSLLLQEFGFPRS 431

Qy        421 KVLKLTRKIDNVETSWALGAIFHYIDSLNRQKSPAS 456
```

```
                 ||||||||||||||||||||||||||||||||||||
Db         432 KVLKLTRKIDNVETSWALGAIFHYIDSLNRQKSPAS 467

RESULT 5
US-10-231-913-124
; Sequence 124, Application US/10231913
; Publication No. US20040005576A1
; GENERAL INFORMATION:
;  APPLICANT: Guo, Xiaojia S.
;  APPLICANT:  Li, Li
;  APPLICANT:  Patturajan, Meera
;  APPLICANT:  Shimkets, Richard A.
;  APPLICANT:  Casman, Stacie J.
;  APPLICANT:  Malyankar, Uriel M.
;  APPLICANT:  Tchernev, Velizar T.
;  APPLICANT:  Vernet, Corine A.
;  APPLICANT:  Spytek, Kimberly A.
;  APPLICANT:  Shenoy, Suresh G.
;  APPLICANT:  Alsobrook II, John P.
;  APPLICANT:  Edinger, Schlomit
;  APPLICANT:  Peyman, John A.
;  APPLICANT:  Stone, David J.
;  APPLICANT:  Ellerman, Karen
;  APPLICANT:  Gangolli, Esha A.
;  APPLICANT:  Boldog, Ference L.
;  APPLICANT:  Colman, Steven D.
;  APPLICANT:  Eisen, Andrew J.
;  APPLICANT:  Liu, Xiaohong
;  APPLICANT:  Padigaru, Muralidhara
;  APPLICANT:  Spaderna, Steven K.
;  APPLICANT:  Zerhusen, Bryan D.
;  TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
;  FILE REFERENCE: 21402-216
;  CURRENT APPLICATION NUMBER: US/10/231,913
;  CURRENT FILING DATE:  2002-08-30
;  PRIOR APPLICATION NUMBER: 60/251,660
;  PRIOR FILING DATE: 2000-12-06
;  PRIOR APPLICATION NUMBER: 60/255,029
;  PRIOR FILING DATE: 2000-12-12
;  PRIOR APPLICATION NUMBER: 60/260,326
;  PRIOR FILING DATE: 2001-01-08
;  PRIOR APPLICATION NUMBER: 60/263,800
;  PRIOR FILING DATE: 2001-01-24
;  PRIOR APPLICATION NUMBER: 60/269,942
;  PRIOR FILING DATE: 2001-02-20
;  PRIOR APPLICATION NUMBER: 60/286,183
;  PRIOR FILING DATE: 2001-04-24
;  PRIOR APPLICATION NUMBER: 60/313,627
;  PRIOR FILING DATE: 2001-08-20
;  PRIOR APPLICATION NUMBER: 60/318,712
;  PRIOR FILING DATE: 2001-09-12
;  NUMBER OF SEQ ID NOS: 292
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 124
;   LENGTH: 484
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-231-913-124

  Query Match             99.7%;  Score 2357;  DB 15;  Length 484;
  Best Local Similarity   99.6%;  Pred. No. 4.1e-217;
  Matches  454;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRKISNHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRATATQAFFSITRAAPGARWGQQAH 60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         29 MRKISNHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRATATQAFFSITRAAPGARWGQQAH 88

Qy         61 SPLGTAADGHEVFYGIMFDAGSTGTRVHVFQFTRPPRETPTLTHETFKAVKPGLSAYADD 120
                |||||||||||||||||||||||||||||||||||||||||||||||||:||||||||||
Db         89 SPLGTAADGHEVFYGIMFDAGSTGTRVHVFQFTRPPRETPTLTHETFKALKPGLSAYADD 148

Qy        121 VEKSAQGIRELLDVAKQDIPFDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASP 180
                |||||||||||||||||||||||||||||||||||||||||||||||||||||:||||||
Db        149 VEKSAQGIRELLDVAKQDIPFDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKKVFKASP 208

Qy        181 FLVGDDCVSIMNGTDEGVSAWITINFLTGSLKTPGGSSVGMLDLGGGSTQIAFLPRVEGT 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        209 FLVGDDCVSIMNGTDEGVSAWITINFLTGSLKTPGGSSVGMLDLGGGSTQIAFLPRVEGT 268

Qy        241 LQASPPGYLTALRMFNRTYKLYSYSYLGLGLMSARLAILGGVEGQPAKDGKELVSPCLSP 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        269 LQASPPGYLTALRMFNRTYKLYSYSYLGLGLMSARLAILGGVEGQPAKDGKELVSPCLSP 328

Qy        301 SFKGEWEHAEVTYRVSGQKAAASLHELCAARVSEVLQNRVHRTEEVKHVDFYAFSYYYDL 360
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        329 SFKGEWEHAEVTYRVSGQKAAASLHELCAARVSEVLQNRVHRTEEVKHVDFYAFSYYYDL 388

Qy        361 AAGVGLIDAEKGGSLVVGDFEIAAKYVCRTLETQPQSSPFSCMDLTYVSLLLQEFGFPRS 420
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        389 AAGVGLIDAEKGGSLVVGDFEIAAKYVCRTLETQPQSSPFSCMDLTYVSLLLQEFGFPRS 448

Qy        421 KVLKLTRKIDNVETSWALGAIFHYIDSLNRQKSPAS 456
                ||||||||||||||||||||||||||||||||||||
Db        449 KVLKLTRKIDNVETSWALGAIFHYIDSLNRQKSPAS 484

RESULT 6
US-10-231-913-38
; Sequence 38, Application US/10231913
; Publication No. US20040005576A1
; GENERAL INFORMATION:
;  APPLICANT: Guo, Xiaojia S.
;  APPLICANT:  Li, Li
;  APPLICANT:  Patturajan, Meera
;  APPLICANT:  Shimkets, Richard A.
;  APPLICANT:  Casman, Stacie J.
;  APPLICANT:  Malyankar, Uriel M.
;  APPLICANT:  Tchernev, Velizar T.
;  APPLICANT:  Vernet, Corine A.
;  APPLICANT:  Spytek, Kimberly A.
;  APPLICANT:  Shenoy, Suresh G.
;  APPLICANT:  Alsobrook II, John P.
;  APPLICANT:  Edinger, Schlomit
;  APPLICANT:  Peyman, John A.
;  APPLICANT:  Stone, David J.
;  APPLICANT:  Ellerman, Karen
;  APPLICANT:  Gangolli, Esha A.
;  APPLICANT:  Boldog, Ference L.
;  APPLICANT:  Colman, Steven D.
;  APPLICANT:  Eisen, Andrew J.
;  APPLICANT:  Liu, Xiaohong
;  APPLICANT:  Padigaru, Muralidhara
;  APPLICANT:  Spaderna, Steven K.
;  APPLICANT:  Zerhusen, Bryan D.
;  TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
;  FILE REFERENCE: 21402-216
;  CURRENT APPLICATION NUMBER: US/10/231,913
;  CURRENT FILING DATE:  2002-08-30
;  PRIOR APPLICATION NUMBER: 60/251,660
;  PRIOR FILING DATE: 2000-12-06
;  PRIOR APPLICATION NUMBER: 60/255,029
;  PRIOR FILING DATE: 2000-12-12
;  PRIOR APPLICATION NUMBER: 60/260,326
;  PRIOR FILING DATE: 2001-01-08
;  PRIOR APPLICATION NUMBER: 60/263,800
;  PRIOR FILING DATE: 2001-01-24
;  PRIOR APPLICATION NUMBER: 60/269,942
;  PRIOR FILING DATE: 2001-02-20
;  PRIOR APPLICATION NUMBER: 60/286,183
;  PRIOR FILING DATE: 2001-04-24
;  PRIOR APPLICATION NUMBER: 60/313,627
;  PRIOR FILING DATE: 2001-08-20
;  PRIOR APPLICATION NUMBER: 60/318,712
;  PRIOR FILING DATE: 2001-09-12
;  NUMBER OF SEQ ID NOS: 292
```

```
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 38
;   LENGTH: 446
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-231-913-38

  Query Match             89.5%;  Score 2116;  DB 15;  Length 446;
  Best Local Similarity   91.0%;  Pred. No. 5.1e-194;
  Matches  415;  Conservative    1;  Mismatches    2;  Indels   38;  Gaps    1;

Qy          1 MRKISNHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRATATQAFFSITRAAPGARWGQQAH 60
              ||||||||||||                                             ||||||||
Db         29 MRKISNHGSLRVAV-------------------------------------ARWGQQAH 50

Qy         61 SPLGTAADGHEVFYGIMFDAGSTGTRVHVFQFTRPPRETPTLTHETFKAVKPGLSAYADD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||:||||||||||
Db         51 SPLGTAADGHEVFYGIMFDAGSTGTRVHVFQFTRPPRETPTLTHETFKALKPGLSAYADD 110

Qy        121 VEKSAQGIRELLDVAKQDIPFDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASP 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db        111 VEKSAQGIRELLDVAKQDIPFDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKGVFKASP 170

Qy        181 FLVGDDCVSIMNGTDEGVSAWITINFLTGSLKTPGGSSVGMLDLGGGSTQIAFLPRVEGT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        171 FLVGDDCVSIMNGTDEGVSAWITINFLTGSLKTPGGSSVGMLDLGGGSTQIAFLPRVEGT 230

Qy        241 LQASPPGYLTALRMFNRTYKLYSYSYLGLGLMSARLAILGGVEGQPAKDGKELVSPCLSP 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        231 LQASPPGYLTALRMFNRTYKLYSYSYLGLGLMSARLAILGGVEGQPAKDGKELVSPCLSP 290

Qy        301 SFKGEWEHAEVTYRVSGQKAAASLHELCAARVSEVLQNRVHRTEEVKHVDFYAFSYYYDL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        291 SFKGEWEHAEVTYRVSGQKAAASLHELCAARVSEVLQNRVHRTEEVKHVDFYAFSYYYDL 350

Qy        361 AAGVGLIDAEKGGSLVVGDFEIAAKYVCRTLETQPQSSPFSCMDLTYVSLLLQEFGFPRS 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        351 AAGVGLIDAEKGGSLVVGDFEIAAKYVCRTLETQPQSSPFSCMDLTYVSLLLQEFGFPRS 410

Qy        421 KVLKLTRKIDNVETSWALGAIFHYIDSLNRQKSPAS 456
              ||||||||||||||||||||||||||||||||||||
Db        411 KVLKLTRKIDNVETSWALGAIFHYIDSLNRQKSPAS 446


RESULT 7
US-10-231-913-125
; Sequence 125, Application US/10231913
; Publication No. US20040005576A1
; GENERAL INFORMATION:
;  APPLICANT: Guo, Xiaojia S.
;  APPLICANT:  Li, Li
;  APPLICANT:  Patturajan, Meera
;  APPLICANT:  Shimkets, Richard A.
;  APPLICANT:  Casman, Stacie J.
;  APPLICANT:  Malyankar, Uriel M.
;  APPLICANT:  Tchernev, Velizar T.
;  APPLICANT:  Vernet, Corine A.
;  APPLICANT:  Spytek, Kimberly A.
;  APPLICANT:  Shenoy, Suresh G.
;  APPLICANT:  Alsobrook II, John P.
;  APPLICANT:  Edinger, Schlomit
;  APPLICANT:  Peyman, John A.
;  APPLICANT:  Stone, David J.
;  APPLICANT:  Ellerman, Karen
;  APPLICANT:  Gangolli, Esha A.
;  APPLICANT:  Boldog, Ference L.
;  APPLICANT:  Colman, Steven D.
;  APPLICANT:  Eisen, Andrew J.
;  APPLICANT:  Liu, Xiaohong
;  APPLICANT:  Padigaru, Muralidhara
;  APPLICANT:  Spaderna, Steven K.
;  APPLICANT:  Zerhusen, Bryan D.
;  TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
;  FILE REFERENCE: 21402-216
;  CURRENT APPLICATION NUMBER: US/10/231,913
;  CURRENT FILING DATE:  2002-08-30
;  PRIOR APPLICATION NUMBER: 60/251,660
;  PRIOR FILING DATE: 2000-12-06
;  PRIOR APPLICATION NUMBER: 60/255,029
;  PRIOR FILING DATE: 2000-12-12
;  PRIOR APPLICATION NUMBER: 60/260,326
;  PRIOR FILING DATE: 2001-01-08
;  PRIOR APPLICATION NUMBER: 60/263,800
;  PRIOR FILING DATE: 2001-01-24
;  PRIOR APPLICATION NUMBER: 60/269,942
;  PRIOR FILING DATE: 2001-02-20
;  PRIOR APPLICATION NUMBER: 60/286,183
;  PRIOR FILING DATE: 2001-04-24
;  PRIOR APPLICATION NUMBER: 60/313,627
;  PRIOR FILING DATE: 2001-08-20
;  PRIOR APPLICATION NUMBER: 60/318,712
;  PRIOR FILING DATE: 2001-09-12
;  NUMBER OF SEQ ID NOS: 292
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 125
;   LENGTH: 455
;   TYPE: PRT
;   ORGANISM: Rattus norvegicus
US-10-231-913-125

  Query Match             87.3%;  Score 2063.5;  DB 15;  Length 455;
  Best Local Similarity   86.6%;  Pred. No. 5.7e-189;
  Matches  394;  Conservative   27;  Mismatches   33;  Indels    1;  Gaps    1;

Qy          1 MRKISNHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRATATQAFFSITRAAPGARWGQQAH 60
              |||| |||:||: |||||||||||:||||||||||:| ||||:|  || | || |||
Db          1 MRKIPNHGTLRMTKVAYPLGLCVGLFIYVAYIKWHRASAAQAFFTIAGAASGVRWTQQAF 60

Qy         61 SPLGTAADGHEVFYGIMFDAGSTGTRVHVFQFTRPPRETPTLTHETFKAVKPGLSAYADD 120
              |   :|  ||||||||||||||||||:||||| ||| ||||||||||:||||||||||
Db         61 SSPDSATRGHEVFYGIMFDAGSTGTRIHVFQFARPPGETPTLTHETFKALKPGLSAYADD 120

Qy        121 VEKSAQGIRELLDVAKQDIPFDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASP 180
              ||||||||:|||:|||| ||:|||||||||||||||||||||||||||||||||||||||
Db        121 VEKSAQGIQELLNVAKQHIPYDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASP 180

Qy        181 FLVGDDCVSIMNGTDEGVSAWITINFLTGSLKTPGGSSVGMLDLGGGSTQIAFLPRVEGT 240
              ||||||||||||||||||||||||:|||||||||| |||||||||||||| ||||||||
Db        181 FLVGDDCVSIMNGTDEGVSAWITVNFLTGSLKTPGSSSVGMLDLGGGSTQITFLPRVEGT 240

Qy        241 LQASPPGYLTALRMFNRTYKLYSYSYLGLGLMSARLAILGGVEGQPAKDGKELVSPCLSP 300
              |||||||:||||:|||||:|||||||||||||||||||||||:||:| ||||||||||
Db        241 LQASPPGHLTALQMFNRTFKLYSYSYLGLGLMSARLAILGGVEGKPAEDDKELVSPCLSP 300

Qy        301 SFKGEWEHAEVTYRVSGQKAAASLHELCAARVSEVLQNRVHRTEEVKHVDFYAFSYYYDL 360
              |:|:|||||||||:|||| |  |:||||:||||||:|:|||||| :|||||||||||||
Db        301 RFRGKWEHAEVTYRISGQK-AVGLYELCASRVSEVLRNKVHRTEEAQHVDFYAFSYYYDL 359

Qy        361 AAGVGLIDAEKGGSLVVGDFEIAAKYVCRTLETQPQSSPFSCMDLTYVSLLLQEFGFPRS 420
              ||  |||||||||||||||||||||||||||||| ||||:||||||:|||| ||||||
Db        360 AASFGLIDAEKGGSLVVGDFEIAAKYVCRTLETQPPSSPFACMDLTYISLLLHEFGFPGD 419

Qy        421 KVLKLTRKIDNVETSWALGAIFHYIDSLNRQKSPA 455
              ||||| |||||||||||||||||||| ||| ||
Db        420 KVLKLARKIDNVETSWALGAIFHYIDSLKRQKVPA 454


RESULT 8
US-10-231-913-271
; Sequence 271, Application US/10231913
; Publication No. US20040005576A1
; GENERAL INFORMATION:
;  APPLICANT: Guo, Xiaojia S.
;  APPLICANT:  Li, Li
;  APPLICANT:  Patturajan, Meera
;  APPLICANT:  Shimkets, Richard A.
```

```
;  APPLICANT:  Casman, Stacie J.
;  APPLICANT:  Malyankar, Uriel M.
;  APPLICANT:  Tchernev, Velizar T.
;  APPLICANT:  Vernet, Corine A.
;  APPLICANT:  Spytek, Kimberly A.
;  APPLICANT:  Shenoy, Suresh G.
;  APPLICANT:  Alsobrook II, John P.
;  APPLICANT:  Edinger, Schlomit
;  APPLICANT:  Peyman, John A.
;  APPLICANT:  Stone, David J.
;  APPLICANT:  Ellerman, Karen
;  APPLICANT:  Gangolli, Esha A.
;  APPLICANT:  Boldog, Ference L.
;  APPLICANT:  Colman, Steven D.
;  APPLICANT:  Eisen, Andrew J.
;  APPLICANT:  Liu, Xiaohong
;  APPLICANT:  Padigaru, Muralidhara
;  APPLICANT:  Spaderna, Steven K.
;  APPLICANT:  Zerhusen, Bryan D.
;  TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
;  FILE REFERENCE: 21402-216
;  CURRENT APPLICATION NUMBER: US/10/231,913
;  CURRENT FILING DATE:  2002-08-30
;  PRIOR APPLICATION NUMBER: 60/251,660
;  PRIOR FILING DATE: 2000-12-06
;  PRIOR APPLICATION NUMBER: 60/255,029
;  PRIOR FILING DATE: 2000-12-12
;  PRIOR APPLICATION NUMBER: 60/260,326
;  PRIOR FILING DATE: 2001-01-08
;  PRIOR APPLICATION NUMBER: 60/263,800
;  PRIOR FILING DATE: 2001-01-24
;  PRIOR APPLICATION NUMBER: 60/269,942
;  PRIOR FILING DATE: 2001-02-20
;  PRIOR APPLICATION NUMBER: 60/286,183
;  PRIOR FILING DATE: 2001-04-24
;  PRIOR APPLICATION NUMBER: 60/313,627
;  PRIOR FILING DATE: 2001-08-20
;  PRIOR APPLICATION NUMBER: 60/318,712
;  PRIOR FILING DATE: 2001-09-12
;  NUMBER OF SEQ ID NOS: 292
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 271
;   LENGTH: 379
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-231-913-271

  Query Match            82.7%;  Score 1954;  DB 15;  Length 379;
  Best Local Similarity  99.7%;  Pred. No. 1.4e-178;
  Matches  378;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         71 EVFYGIMFDAGSTGTRVHVFQFTRPPRETPTLTHETFKAVKPGLSAYADDVEKSAQGIRE 130
              ||||||||||||||||||||||||||||||||||||||||:|||||||||||||||||||
Db          1 EVFYGIMFDAGSTGTRVHVFQFTRPPRETPTLTHETFKALKPGLSAYADDVEKSAQGIRE 60

Qy        131 LLDVAKQDIPFDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASPFLVGDDCVSI 190
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LLDVAKQDIPFDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASPFLVGDDCVSI 120

Qy        191 MNGTDEGVSAWITINFLTGSLKTPGGSSVGMLDLGGGSTQIAFLPRVEGTLQASPPGYLT 250
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 MNGTDEGVSAWITINFLTGSLKTPGGSSVGMLDLGGGSTQIAFLPRVEGTLQASPPGYLT 180

Qy        251 ALRMFNRTYKLYSYSYLGLGLMSARLAILGGVEGQPAKDGKELVSPCLSPSFKGEWEHAE 310
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ALRMFNRTYKLYSYSYLGLGLMSARLAILGGVEGQPAKDGKELVSPCLSPSFKGEWEHAE 240

Qy        311 VTYRVSGQKAAASLHELCAARVSEVLQNRVHRTEEVKHVDFYAFSYYYDLAAGVGLIDAE 370
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 VTYRVSGQKAAASLHELCAARVSEVLQNRVHRTEEVKHVDFYAFSYYYDLAAGVGLIDAE 300

Qy        371 KGGSLVVGDFEIAAKYVCRTLETQPQSSPFSCMDLTYVSLLLQEFGFPRSKVLKLTRKID 430
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 KGGSLVVGDFEIAAKYVCRTLETQPQSSPFSCMDLTYVSLLLQEFGFPRSKVLKLTRKID 360

Qy        431 NVETSWALGAIFHYIDSLN 449
              |||||||||||||||||||
Db        361 NVETSWALGAIFHYIDSLN 379


RESULT 9
US-10-231-913-126
; Sequence 126, Application US/10231913
; Publication No. US20040005576A1
; GENERAL INFORMATION:
;  APPLICANT: Guo, Xiaojia S.
;  APPLICANT:  Li, Li
;  APPLICANT:  Patturajan, Meera
;  APPLICANT:  Shimkets, Richard A.
;  APPLICANT:  Casman, Stacie J.
;  APPLICANT:  Malyankar, Uriel M.
;  APPLICANT:  Tchernev, Velizar T.
;  APPLICANT:  Vernet, Corine A.
;  APPLICANT:  Spytek, Kimberly A.
;  APPLICANT:  Shenoy, Suresh G.
;  APPLICANT:  Alsobrook II, John P.
;  APPLICANT:  Edinger, Schlomit
;  APPLICANT:  Peyman, John A.
;  APPLICANT:  Stone, David J.
;  APPLICANT:  Ellerman, Karen
;  APPLICANT:  Gangolli, Esha A.
;  APPLICANT:  Boldog, Ference L.
;  APPLICANT:  Colman, Steven D.
;  APPLICANT:  Eisen, Andrew J.
;  APPLICANT:  Liu, Xiaohong
;  APPLICANT:  Padigaru, Muralidhara
;  APPLICANT:  Spaderna, Steven K.
;  APPLICANT:  Zerhusen, Bryan D.
;  TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
;  FILE REFERENCE: 21402-216
;  CURRENT APPLICATION NUMBER: US/10/231,913
;  CURRENT FILING DATE:  2002-08-30
;  PRIOR APPLICATION NUMBER: 60/251,660
;  PRIOR FILING DATE: 2000-12-06
;  PRIOR APPLICATION NUMBER: 60/255,029
;  PRIOR FILING DATE: 2000-12-12
;  PRIOR APPLICATION NUMBER: 60/260,326
;  PRIOR FILING DATE: 2001-01-08
;  PRIOR APPLICATION NUMBER: 60/263,800
;  PRIOR FILING DATE: 2001-01-24
;  PRIOR APPLICATION NUMBER: 60/269,942
;  PRIOR FILING DATE: 2001-02-20
;  PRIOR APPLICATION NUMBER: 60/286,183
;  PRIOR FILING DATE: 2001-04-24
;  PRIOR APPLICATION NUMBER: 60/313,627
;  PRIOR FILING DATE: 2001-08-20
;  PRIOR APPLICATION NUMBER: 60/318,712
;  PRIOR FILING DATE: 2001-09-12
;  NUMBER OF SEQ ID NOS: 292
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 126
;   LENGTH: 427
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-10-231-913-126

  Query Match            42.6%;  Score 1007;  DB 15;  Length 427;
  Best Local Similarity  50.0%;  Pred. No. 1.5e-87;
  Matches  213;  Conservative   62;  Mismatches  133;  Indels   18;  Gaps    6;

Qy         37 ATATQAFFSITRAAPGA--------RWGQ----QAHSPLGTAADGHEVFYGIMFDAGSTG 84
              ||:  | | :  |  |:          | :     :  |:  :|     ||||||||||||
Db          2 ATSWGAVFMLIIACVGSTVFYREQQTWFEGVFLSSMCPINVSAG---TFYGIMFDAGSTG 58

Qy         85 TRVHVFQFT-RPPRETPTLTHETFKAVKPGLSAYADDVEKSAQGIRELLDVAKQDIPFDF 143
              ||:||: |  :   : | |  | | :||||||: |  :: |: ::|||:|||  ||
```

```
Db          59 TRIHVYTFVQKTAGQLPFLEGEIFDSVKPGLSAFVDQPKQGAETVQELLEVAKDSIPRSH 118

Qy         144 WKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASPFLVGDDCVSIMNGTDEGVSAWIT 203

Db         119 WERTPVVLKATAGLRLLPEQKAQALLLEVEEIFKNSPFLVPDGSVSIMDGSYEGILAWVT 178

Qy         204 INFLTGSLKTPGGSSVGMLDLGGGSTQIAFLPRVEGTLQASPPGYLTALRMFNRTYKLYS 263

Db         179 VNFLTGQLHGRGQETVGTLDLGGASTQITFLPQFEKTLEQTPRGYLTSFEMFNSTFKLYT 238

Qy         264 YSYLGLGLMSARLAILGGVEGQPAKDGKELVSPCLSPSFKGEWEHAEVTYRVSGQKAAAS 323

Db         239 HSYLGFGLKAARLATLGALEAK-GTDGHTFRSACLPRWLEAEWIFGGVKYQYGGNQEGEM 297

Qy         324 LHELCAARVSEVLQNRVHRTEEVKHVDFYAFSYYYDLAAGVGLIDAEKGGSLVVGDFEIA 383

Db         298 GFEPCYAEVLRVVQGKLHQPEEVRGSAFYAFSYYYDRAADTHLIDYEKGGVLKVEDFERK 357

Qy         384 AKYVCRTLETQPQSSPFSCMDLTYVSLLLQE-FGFPRSKVLKLTRKIDNVETSWALGAIF 442

Db         358 AREVCDNLGSFSSGSPFLCMDLTYITALLKDGFGFADGTLLQLTKKVNNIETGWALGATF 417

Qy         443 HYIDSL 448

Db         418 HLLQSL 423


RESULT 10
US-10-091-085-3
; Sequence 3, Application US/10091085
; Publication No. US20020146772A1
; GENERAL INFORMATION:
;  APPLICANT: Ford, John
;  APPLICANT:  Mulero, Julio
;  TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE
;  TITLE OF INVENTION:  POLYPEPTIDES
;  FILE REFERENCE: 28110/35761
;  CURRENT APPLICATION NUMBER: US/10/091,085
;  CURRENT FILING DATE:  2002-03-05
;  PRIOR APPLICATION NUMBER: 09/350,836
;  PRIOR FILING DATE: 1999-07-09
;  PRIOR APPLICATION NUMBER: 09/273,447
;  PRIOR FILING DATE: 1999-03-19
;  PRIOR APPLICATION NUMBER: 09/118,205
;  PRIOR FILING DATE: 1998-07-16
;  PRIOR APPLICATION NUMBER: 09/122,449
;  PRIOR FILING DATE: 1998-07-24
;  PRIOR APPLICATION NUMBER: 09/244,444
;  PRIOR FILING DATE: 1999-02-04
;  NUMBER OF SEQ ID NOS: 23
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
;   LENGTH: 428
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-091-085-3

  Query Match           42.3%;  Score 999;  DB 13;  Length 428;
  Best Local Similarity  52.4%;  Pred. No. 8.8e-87;
  Matches  204;  Conservative   56;  Mismatches  123;  Indels    6;  Gaps    4;

Qy          62 PLGTAADGHEVFYGIMFDAGSTGTRVHVFQFT-RPPRETPTLTHETFKAVKPGLSAYADD 120

Db          40 PINVSA---STLYGIMFDAGSTGTRIHVYTFVQKMPGQLPILEGEVFDSVKPGLSAFVDQ 96

Qy         121 VEKSAQGIRELLDVAKQDIPFDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASP 180

Db          97 PKQGAETVQGLLEVAKDSIPRSHWKKTPVVLKATAGLRLLPEHKAKALLFEVKEIFRKSP 156

Qy         181 FLVGDDCVSIMNGTDEGVSAWITINFLTGSLKTPGGSSVGMLDLGGGSTQIAFLPRVEGT 240

Db         157 FLVPKGSVSIMDGSDEGILAWVTVNFLTGQLHGHRQETVGTLDLGGASTQITFLPQFEKT 216

Qy         241 LQASPPGYLTALRMFNRTYKLYSYSYLGLGLMSARLAILGGVEGQPAKDGKELVSPCLSP 300

Db         217 LEQTPRGYLTSFEMFNSTYKLYTHSYLGFGLKAARLATLGALETE-GTDGHTFRSACLPR 275

Qy         301 SFKGEWEHAEVTYRVSGQKAAASLHELCAARVSEVLQNRVHRTEEVKHVDFYAFSYYYDL 360

Db         276 WLEAEWIFGGVKYQYGGNQEGEVGFEPCYAEVLRVVRGKLHQPEEVQRGSFYAFSYYYDR 335

Qy         361 AAGVGLIDAEKGGSLVVGDFEIAAKYVCRTLETQPQSSPFSCMDLTYVSLLLQE-FGFPR 419

Db         336 AVDTDMIDYEKGGILKVEDFERKAREVCDNLENFTSGSPFLCMDLSYITALLKDGFGFAD 395

Qy         420 SKVLKLTRKIDNVETSWALGAIFHYIDSL 448

Db         396 STVLQLTKKVNNIETGWALGATFHLLQSL 424


RESULT 11
US-10-091-085-5
; Sequence 5, Application US/10091085
; Publication No. US20020146772A1
; GENERAL INFORMATION:
;  APPLICANT: Ford, John
;  APPLICANT:  Mulero, Julio
;  TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE
;  TITLE OF INVENTION:  POLYPEPTIDES
;  FILE REFERENCE: 28110/35761
;  CURRENT APPLICATION NUMBER: US/10/091,085
;  CURRENT FILING DATE:  2002-03-05
;  PRIOR APPLICATION NUMBER: 09/350,836
;  PRIOR FILING DATE: 1999-07-09
;  PRIOR APPLICATION NUMBER: 09/273,447
;  PRIOR FILING DATE: 1999-03-19
;  PRIOR APPLICATION NUMBER: 09/118,205
;  PRIOR FILING DATE: 1998-07-16
;  PRIOR APPLICATION NUMBER: 09/122,449
;  PRIOR FILING DATE: 1998-07-24
;  PRIOR APPLICATION NUMBER: 09/244,444
;  PRIOR FILING DATE: 1999-02-04
;  NUMBER OF SEQ ID NOS: 23
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
;   LENGTH: 428
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-091-085-5

  Query Match           42.3%;  Score 999;  DB 13;  Length 428;
  Best Local Similarity  52.4%;  Pred. No. 8.8e-87;
  Matches  204;  Conservative   56;  Mismatches  123;  Indels    6;  Gaps    4;

Qy          62 PLGTAADGHEVFYGIMFDAGSTGTRVHVFQFT-RPPRETPTLTHETFKAVKPGLSAYADD 120

Db          40 PINVSA---STLYGIMFDAGSTGTRIHVYTFVQKMPGQLPILEGEVFDSVKPGLSAFVDQ 96

Qy         121 VEKSAQGIRELLDVAKQDIPFDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASP 180

Db          97 PKQGAETVQGLLEVAKDSIPRSHWKKTPVVLKATAGLRLLPEHKAKALLFEVKEIFRKSP 156

Qy         181 FLVGDDCVSIMNGTDEGVSAWITINFLTGSLKTPGGSSVGMLDLGGGSTQIAFLPRVEGT 240

Db         157 FLVPKGSVSIMDGSDEGILAWVTVNFLTGQLHGHRQETVGTLDLGGASTQITFLPQFEKT 216

Qy         241 LQASPPGYLTALRMFNRTYKLYSYSYLGLGLMSARLAILGGVEGQPAKDGKELVSPCLSP 300

Db         217 LEQTPRGYLTSFEMFNSTYKLYTHSYLGFGLKAARLATLGALETE-GTDGHTFRSACLPR 275

Qy         301 SFKGEWEHAEVTYRVSGQKAAASLHELCAARVSEVLQNRVHRTEEVKHVDFYAFSYYYDL 360

Db         276 WLEAEWIFGGVKYQYGGNQEGEVGFEPCYAEVLRVVRGKLHQPEEVQRGSFYAFSYYYDR 335

Qy         361 AAGVGLIDAEKGGSLVVGDFEIAAKYVCRTLETQPQSSPFSCMDLTYVSLLLQE-FGFPR 419

Db         336 AVDTDMIDYEKGGILKVEDFERKAREVCDNLENFTSGSPFLCMDLSYITALLKDGFGFAD 395

Qy         420 SKVLKLTRKIDNVETSWALGAIFHYIDSL 448

Db         396 STVLQLTKKVNNIETGWALGATFHLLQSL 424
```

```
Db        336 AVDTDMIDYEKGGILKVEDFERKAREVCDNLENFTSGSPFLCMDLSYITALLKDGFGFAD 395

Qy        420 SKVLKLTRKIDNVETSWALGAIFHYIDSL 448
              | ||:||:|::|:|| ||||| || : ||
Db        396 STVLQLTKKVNNIETGWALGATFHLLQSL 424


RESULT 12
US-10-092-063-3
; Sequence 3, Application US/10092063
; Publication No. US20020173005A1
; GENERAL INFORMATION:
;  APPLICANT: Ford, John
;  APPLICANT:  Mulero, Julio
;  TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE POLYPEPTIDES
;  FILE REFERENCE: 28110/35908
;  CURRENT APPLICATION NUMBER: US/10/092,063
;  CURRENT FILING DATE:  2002-03-05
;  PRIOR APPLICATION NUMBER: 09/370,265
;  PRIOR FILING DATE: 2002-01-31
;  PRIOR APPLICATION NUMBER: PCT/US99/16180
;  PRIOR FILING DATE: 1999-07-16
;  PRIOR APPLICATION NUMBER: 09/350,836
;  PRIOR FILING DATE: 1999-07-09
;  PRIOR APPLICATION NUMBER: 09/273,447
;  PRIOR FILING DATE: 1999-03-19
;  PRIOR APPLICATION NUMBER: 09/244,444
;  PRIOR FILING DATE: 1999-02-04
;  PRIOR APPLICATION NUMBER: 09/122,449
;  PRIOR FILING DATE: 1998-07-24
;  PRIOR APPLICATION NUMBER: 09/118,205
;  PRIOR FILING DATE: 1998-07-16
;  NUMBER OF SEQ ID NOS: 39
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
;   LENGTH: 428
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-092-063-3

  Query Match            42.3%;  Score 999;  DB 13;  Length 428;
  Best Local Similarity  52.4%;  Pred. No. 8.8e-87;
  Matches  204;  Conservative   56;  Mismatches  123;  Indels    6;  Gaps    4;

Qy         62 PLGTAADGHEVFYGIMFDAGSTGTRVHVFQFT-RPPRETPTLTHETFKAVKPGLSAYADD 120
              |:  :|       |||||||||||||:||: |  : | :  |  | | :|||||||: |
Db         40 PINVSA---STLYGIMFDAGSTGTRIHVYTFVQKMPGQLPILEGEVFDSVKPGLSAFVDQ 96

Qy        121 VEKSAQGIRELLDVAKQDIPFDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASP 180
               :: |: :: ||:|||  ||   || ||:|||||||||||||  ||: || :|||:|: ||
Db         97 PKQGAETVQGLLEVAKDSIPRSHWKKTPVVLKATAGLRLLPEHKAKALLFEVKEIFRKSP 156

Qy        181 FLVGDDCVSIMNGTDEGVSAWITINFLTGSLKTPGGSSVGMLDLGGGSTQIAFLPRVEGT 240
              |||     ||||:|:|||: ||:|:|||||  |       :|| ||||| |||| |||: | |
Db        157 FLVPKGSVSIMDGSDEGILAWVTVNFLTGQLHGHRQETVGTLDLGGASTQITFLPQFEKT 216

Qy        241 LQASPPGYLTALRMFNRTYKLYSYSYLGLGLMSARLAILGGVEGQPAKDGKELVSPCLSP 300
              |: :| ||||:  ||| |||||::|||| || :|||| || :| :   ||    | ||
Db        217 LEQTPRGYLTSFEMFNSTYKLYTHSYLGFGLKAARLATLGALETE-GTDGHTFRSACLPR 275

Qy        301 SFKGEWEHAEVTYRVSGQKAAASLHELCAARVSEVLQNRVHRTEEVKHVDFYAFSYYYDL 360
              : ||    | |:  | :       | | | |  |:: ::|: |||:   |||||||||
Db        276 WLEAEWIFGGVKYQYGGNQEGEVGFEPCYAEVLRVVRGKLHQPEEVQRGSFYAFSYYYDR 335

Qy        361 AAGVGLIDAEKGGSLVVGDFEIAAKYVCRTLETQPQSSPFSCMDLTYVSLLLQE-FGFPR 419
              |    :|| |||| | | |||  |: ||  ||     ||| ||||:|:: ||:: |||
Db        336 AVDTDMIDYEKGGILKVEDFERKAREVCDNLENFTSGSPFLCMDLSYITALLKDGFGFAD 395

Qy        420 SKVLKLTRKIDNVETSWALGAIFHYIDSL 448
              | ||:||:|::|:|| ||||| || : ||
Db        396 STVLQLTKKVNNIETGWALGATFHLLQSL 424


RESULT 13
US-10-092-063-5
; Sequence 5, Application US/10092063
; Publication No. US20020173005A1
; GENERAL INFORMATION:
;  APPLICANT: Ford, John
;  APPLICANT:  Mulero, Julio
;  TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE POLYPEPTIDES
;  FILE REFERENCE: 28110/35908
;  CURRENT APPLICATION NUMBER: US/10/092,063
;  CURRENT FILING DATE:  2002-03-05
;  PRIOR APPLICATION NUMBER: 09/370,265
;  PRIOR FILING DATE: 2002-01-31
;  PRIOR APPLICATION NUMBER: PCT/US99/16180
;  PRIOR FILING DATE: 1999-07-16
;  PRIOR APPLICATION NUMBER: 09/350,836
;  PRIOR FILING DATE: 1999-07-09
;  PRIOR APPLICATION NUMBER: 09/273,447
;  PRIOR FILING DATE: 1999-03-19
;  PRIOR APPLICATION NUMBER: 09/244,444
;  PRIOR FILING DATE: 1999-02-04
;  PRIOR APPLICATION NUMBER: 09/122,449
;  PRIOR FILING DATE: 1998-07-24
;  PRIOR APPLICATION NUMBER: 09/118,205
;  PRIOR FILING DATE: 1998-07-16
;  NUMBER OF SEQ ID NOS: 39
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
;   LENGTH: 428
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-092-063-5

  Query Match            42.3%;  Score 999;  DB 13;  Length 428;
  Best Local Similarity  52.4%;  Pred. No. 8.8e-87;
  Matches  204;  Conservative   56;  Mismatches  123;  Indels    6;  Gaps    4;

Qy         62 PLGTAADGHEVFYGIMFDAGSTGTRVHVFQFT-RPPRETPTLTHETFKAVKPGLSAYADD 120
              |:  :|       |||||||||||||:||: |  : | :  |  | | :|||||||: |
Db         40 PINVSA---STLYGIMFDAGSTGTRIHVYTFVQKMPGQLPILEGEVFDSVKPGLSAFVDQ 96

Qy        121 VEKSAQGIRELLDVAKQDIPFDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASP 180
               :: |: :: ||:|||  ||   || ||:|||||||||||||  ||: || :|||:|: ||
Db         97 PKQGAETVQGLLEVAKDSIPRSHWKKTPVVLKATAGLRLLPEHKAKALLFEVKEIFRKSP 156

Qy        181 FLVGDDCVSIMNGTDEGVSAWITINFLTGSLKTPGGSSVGMLDLGGGSTQIAFLPRVEGT 240
              |||     ||||:|:|||: ||:|:|||||  |       :|| ||||| |||| |||: | |
Db        157 FLVPKGSVSIMDGSDEGILAWVTVNFLTGQLHGHRQETVGTLDLGGASTQITFLPQFEKT 216

Qy        241 LQASPPGYLTALRMFNRTYKLYSYSYLGLGLMSARLAILGGVEGQPAKDGKELVSPCLSP 300
              |: :| ||||:  ||| |||||::|||| || :|||| || :| :   ||    | ||
Db        217 LEQTPRGYLTSFEMFNSTYKLYTHSYLGFGLKAARLATLGALETE-GTDGHTFRSACLPR 275

Qy        301 SFKGEWEHAEVTYRVSGQKAAASLHELCAARVSEVLQNRVHRTEEVKHVDFYAFSYYYDL 360
              : ||    | |:  | :       | | | |  |:: ::|: |||:   |||||||||
Db        276 WLEAEWIFGGVKYQYGGNQEGEVGFEPCYAEVLRVVRGKLHQPEEVQRGSFYAFSYYYDR 335

Qy        361 AAGVGLIDAEKGGSLVVGDFEIAAKYVCRTLETQPQSSPFSCMDLTYVSLLLQE-FGFPR 419
              |    :|| |||| | | |||  |: ||  ||     ||| ||||:|:: ||:: |||
Db        336 AVDTDMIDYEKGGILKVEDFERKAREVCDNLENFTSGSPFLCMDLSYITALLKDGFGFAD 395

Qy        420 SKVLKLTRKIDNVETSWALGAIFHYIDSL 448
              | ||:||:|::|:|| ||||| || : ||
Db        396 STVLQLTKKVNNIETGWALGATFHLLQSL 424


RESULT 14
US-10-286-926-3
; Sequence 3, Application US/10286926
; Publication No. US20030175752A1
; GENERAL INFORMATION:
;  APPLICANT: Ford, John
;  APPLICANT:  Mulero, Julio
```

```
;  APPLICANT:  Yeung, George
;  TITLE OF INVENTION: Methods and Materials Relating to CD39-Like
;  TITLE OF INVENTION:  Polypeptides
;  FILE REFERENCE: 28110/36457CON
;  CURRENT APPLICATION NUMBER: US/10/286,926
;  CURRENT FILING DATE:  2002-11-01
;  PRIOR APPLICATION NUMBER: 09/557,800
;  PRIOR FILING DATE: 2000-04-25
;  PRIOR APPLICATION NUMBER: 09/481,238
;  PRIOR FILING DATE: 2000-01-11
;  PRIOR APPLICATION NUMBER: 09/370,265
;  PRIOR FILING DATE: 1999-08-09
;  PRIOR APPLICATION NUMBER: PCT/US99/16180
;  PRIOR FILING DATE: 1999-07-16
;  PRIOR APPLICATION NUMBER: 09/350836
;  PRIOR FILING DATE: 1999-07-09
;  PRIOR APPLICATION NUMBER: 09/273447
;  PRIOR FILING DATE: 1999-03-19
;  PRIOR APPLICATION NUMBER: 09/122449
;  PRIOR FILING DATE: 1998-07-24
;  PRIOR APPLICATION NUMBER: 09/244444
;  PRIOR FILING DATE: 1999-02-04
;  PRIOR APPLICATION NUMBER: 09/118,205
;  PRIOR FILING DATE: 1998-07-16
;  NUMBER OF SEQ ID NOS: 54
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
;   LENGTH: 428
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-286-926-3

  Query Match           42.3%;  Score 999;  DB 14;  Length 428;
  Best Local Similarity  52.4%;  Pred. No. 8.8e-87;
  Matches  204;  Conservative   56;  Mismatches  123;  Indels    6;  Gaps    4;

Qy         62 PLGTAADGHEVFYGIMFDAGSTGTRVHVFQFT-RPPRETPTLTHETFKAVKPGLSAYADD 120
              |:  :|      ||||||||||||||:||: |  : | : | |  | | :|||||||: |
Db         40 PINVSA---STLYGIMFDAGSTGTRIHVYTFVQKMPGQLPILEGEVFDSVKPGLSAFVDQ 96

Qy        121 VEKSAQGIRELLDVAKQDIPFDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASP 180
               :: |: :: ||:|||  ||   || ||:|||||||||||  ||: || :|||:|: ||
Db         97 PKQGAETVQGLLEVAKDSIPRSHWKKTPVVLKATAGLRLLPEHKAKALLFEVKEIFRKSP 156

Qy        181 FLVGDDCVSIMNGTDEGVSAWITINFLTGSLKTPGGSSVGMLDLGGGSTQIAFLPRVEGT 240
              |||    ||||:|:|||: ||:|:|||||  |      :|| ||||| |||| |||: | |
Db        157 FLVPKGSVSIMDGSDEGILAWVTVNFLTGQLHGHRQETVGTLDLGGASTQITFLPQFEKT 216

Qy        241 LQASPPGYLTALRMFNRTYKLYSYSYLGLGLMSARLAILGGVEGQPAKDGKELVSPCLSP 300
              |: :| ||||:  ||| |||||::|||| || :|||| || :| :   ||    | ||
Db        217 LEQTPRGYLTSFEMFNSTYKLYTHSYLGFGLKAARLATLGALETE-GTDGHTFRSACLPR 275

Qy        301 SFKGEWEHAEVTYRVSGQKAAASLHELCAARVSEVLQNRVHRTEEVKHVDFYAFSYYYDL 360
              : ||    | |:  | :       | | | |  |:: ::|: |||:   |||||||||
Db        276 WLEAEWIFGGVKYQYGGNQEGEVGFEPCYAEVLRVVRGKLHQPEEVQRGSFYAFSYYYDR 335

Qy        361 AAGVGLIDAEKGGSLVVGDFEIAAKYVCRTLETQPQSSPFSCMDLTYVSLLLQE-FGFPR 419
              |    :|| |||| | | |||  |: ||  ||     ||| ||||:|:: ||:: |||
Db        336 AVDTDMIDYEKGGILKVEDFERKAREVCDNLENFTSGSPFLCMDLSYITALLKDGFGFAD 395

Qy        420 SKVLKLTRKIDNVETSWALGAIFHYIDSL 448
              | ||:||:|::|:|| ||||| || : ||
Db        396 STVLQLTKKVNNIETGWALGATFHLLQSL 424


RESULT 15
US-10-286-926-5
; Sequence 5, Application US/10286926
; Publication No. US20030175752A1
; GENERAL INFORMATION:
;  APPLICANT: Ford, John
;  APPLICANT:  Mulero, Julio
;  APPLICANT:  Yeung, George
;  TITLE OF INVENTION: Methods and Materials Relating to CD39-Like
;  TITLE OF INVENTION:  Polypeptides
;  FILE REFERENCE: 28110/36457CON
;  CURRENT APPLICATION NUMBER: US/10/286,926
;  CURRENT FILING DATE:  2002-11-01
;  PRIOR APPLICATION NUMBER: 09/557,800
;  PRIOR FILING DATE: 2000-04-25
;  PRIOR APPLICATION NUMBER: 09/481,238
;  PRIOR FILING DATE: 2000-01-11
;  PRIOR APPLICATION NUMBER: 09/370,265
;  PRIOR FILING DATE: 1999-08-09
;  PRIOR APPLICATION NUMBER: PCT/US99/16180
;  PRIOR FILING DATE: 1999-07-16
;  PRIOR APPLICATION NUMBER: 09/350836
;  PRIOR FILING DATE: 1999-07-09
;  PRIOR APPLICATION NUMBER: 09/273447
;  PRIOR FILING DATE: 1999-03-19
;  PRIOR APPLICATION NUMBER: 09/122449
;  PRIOR FILING DATE: 1998-07-24
;  PRIOR APPLICATION NUMBER: 09/244444
;  PRIOR FILING DATE: 1999-02-04
;  PRIOR APPLICATION NUMBER: 09/118,205
;  PRIOR FILING DATE: 1998-07-16
;  NUMBER OF SEQ ID NOS: 54
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
;   LENGTH: 428
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-286-926-5

  Query Match           42.3%;  Score 999;  DB 14;  Length 428;
  Best Local Similarity  52.4%;  Pred. No. 8.8e-87;
  Matches  204;  Conservative   56;  Mismatches  123;  Indels    6;  Gaps    4;

Qy         62 PLGTAADGHEVFYGIMFDAGSTGTRVHVFQFT-RPPRETPTLTHETFKAVKPGLSAYADD 120
              |:  :|      ||||||||||||||:||: |  : | : | |  | | :|||||||: |
Db         40 PINVSA---STLYGIMFDAGSTGTRIHVYTFVQKMPGQLPILEGEVFDSVKPGLSAFVDQ 96

Qy        121 VEKSAQGIRELLDVAKQDIPFDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASP 180
               :: |: :: ||:|||  ||   || ||:|||||||||||  ||: || :|||:|: ||
Db         97 PKQGAETVQGLLEVAKDSIPRSHWKKTPVVLKATAGLRLLPEHKAKALLFEVKEIFRKSP 156

Qy        181 FLVGDDCVSIMNGTDEGVSAWITINFLTGSLKTPGGSSVGMLDLGGGSTQIAFLPRVEGT 240
              |||    ||||:|:|||: ||:|:|||||  |      :|| ||||| |||| |||: | |
Db        157 FLVPKGSVSIMDGSDEGILAWVTVNFLTGQLHGHRQETVGTLDLGGASTQITFLPQFEKT 216

Qy        241 LQASPPGYLTALRMFNRTYKLYSYSYLGLGLMSARLAILGGVEGQPAKDGKELVSPCLSP 300
              |: :| ||||:  ||| |||||::|||| || :|||| || :| :   ||    | ||
Db        217 LEQTPRGYLTSFEMFNSTYKLYTHSYLGFGLKAARLATLGALETE-GTDGHTFRSACLPR 275

Qy        301 SFKGEWEHAEVTYRVSGQKAAASLHELCAARVSEVLQNRVHRTEEVKHVDFYAFSYYYDL 360
              : ||    | |:  | :       | | | |  |:: ::|: |||:   |||||||||
Db        276 WLEAEWIFGGVKYQYGGNQEGEVGFEPCYAEVLRVVRGKLHQPEEVQRGSFYAFSYYYDR 335

Qy        361 AAGVGLIDAEKGGSLVVGDFEIAAKYVCRTLETQPQSSPFSCMDLTYVSLLLQE-FGFPR 419
              |    :|| |||| | | |||  |: ||  ||     ||| ||||:|:: ||:: |||
Db        336 AVDTDMIDYEKGGILKVEDFERKAREVCDNLENFTSGSPFLCMDLSYITALLKDGFGFAD 395

Qy        420 SKVLKLTRKIDNVETSWALGAIFHYIDSL 448
              | ||:||:|::|:|| ||||| || : ||
Db        396 STVLQLTKKVNNIETGWALGATFHLLQSL 424


Search completed: November 16, 2004, 17:12:01
Job time : 144 secs
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: November 16, 2004, 16:38:51 ; Search time 40 Seconds
(without alignments)
756.025 Million cell updates/sec

Title: US-09-905-589A-2
Perfect score: 2364
Sequence: 1 MRKISNHGSLRVAKVAYPLG.....ALGAIFHYIDSLNRQKSPAS 456

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2364	100.0	456	3	US-09-240-639-2	Sequence 2, Appli
2	2364	100.0	456	4	US-09-908-510A-2	Sequence 2, Appli
3	2364	100.0	456	4	US-09-905-744-2	Sequence 2, Appli
4	2364	100.0	456	4	US-10-107-660-2	Sequence 2, Appli
5	2364	100.0	456	4	US-10-107-576-2	Sequence 2, Appli
6	2364	100.0	456	4	US-09-905-732-2	Sequence 2, Appli
7	2364	100.0	484	3	US-09-608-285A-27	Sequence 27, Appl
8	2364	100.0	484	4	US-09-370-265-27	Sequence 27, Appl
9	2364	100.0	484	4	US-09-557-800C-27	Sequence 27, Appl
10	2364	100.0	484	4	US-09-370-625A-27	Sequence 27, Appl
11	2003	84.7	471	3	US-09-608-285A-60	Sequence 60, Appl
12	999	42.3	428	3	US-09-608-285A-3	Sequence 3, Appli
13	999	42.3	428	3	US-09-608-285A-5	Sequence 5, Appli
14	999	42.3	428	3	US-09-240-639-6	Sequence 6, Appli
15	999	42.3	428	3	US-09-240-639-9	Sequence 9, Appli
16	999	42.3	428	3	US-09-350-836B-3	Sequence 3, Appli
17	999	42.3	428	3	US-09-350-836B-5	Sequence 5, Appli
18	999	42.3	428	4	US-09-370-265-3	Sequence 3, Appli
19	999	42.3	428	4	US-09-370-265-5	Sequence 5, Appli
20	999	42.3	428	4	US-09-557-800C-3	Sequence 3, Appli
21	999	42.3	428	4	US-09-557-800C-5	Sequence 5, Appli
22	999	42.3	428	4	US-09-370-625A-3	Sequence 3, Appli
23	999	42.3	428	4	US-09-370-625A-5	Sequence 5, Appli
24	999	42.3	428	4	US-09-908-510A-6	Sequence 6, Appli
25	999	42.3	428	4	US-09-908-510A-9	Sequence 9, Appli
26	999	42.3	428	4	US-09-905-744-6	Sequence 6, Appli
27	999	42.3	428	4	US-09-905-744-9	Sequence 9, Appli
28	999	42.3	428	4	US-10-107-660-6	Sequence 6, Appli
29	999	42.3	428	4	US-10-107-660-9	Sequence 9, Appli
30	999	42.3	428	4	US-10-107-576-6	Sequence 6, Appli
31	999	42.3	428	4	US-10-107-576-9	Sequence 9, Appli
32	999	42.3	428	4	US-09-905-732-6	Sequence 6, Appli
33	999	42.3	428	4	US-09-905-732-9	Sequence 9, Appli
34	996	42.1	428	3	US-09-608-285A-7	Sequence 7, Appli
35	996	42.1	428	3	US-09-350-836B-7	Sequence 7, Appli
36	996	42.1	428	4	US-09-370-265-7	Sequence 7, Appli
37	996	42.1	428	4	US-09-557-800C-7	Sequence 7, Appli
38	996	42.1	428	4	US-09-370-625A-7	Sequence 7, Appli
39	909	38.5	405	3	US-09-608-285A-25	Sequence 25, Appl
40	909	38.5	405	4	US-09-370-265-25	Sequence 25, Appl
41	909	38.5	405	4	US-09-557-800C-25	Sequence 25, Appl
42	909	38.5	405	4	US-09-370-625A-25	Sequence 25, Appl
43	909	38.5	465	4	US-09-557-800C-56	Sequence 56, Appl
44	909	38.5	465	4	US-09-370-625A-39	Sequence 39, Appl
45	904	38.2	465	3	US-09-240-639-8	Sequence 8, Appli

ALIGNMENTS

RESULT 1
US-09-240-639-2
; Sequence 2, Application US/09240639
; Patent No. 6350447
; GENERAL INFORMATION:
; APPLICANT: Chadwick, Brian Paul
; APPLICANT: Frischauf, Anna-Maria
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE
; TITLE OF INVENTION: POLYPEPTIDES AND NUCLEIC ACIDS
; FILE REFERENCE: 9598-066
; CURRENT APPLICATION NUMBER: US/09/240,639
; CURRENT FILING DATE: 1998-01-29
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 456
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-240-639-2

Query Match 100.0%; Score 2364; DB 3; Length 456;
Best Local Similarity 100.0%; Pred. No. 1.1e-230;
Matches 456; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MRKISNHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRATATQAFFSITRAAPGARWGQQAH 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRKISNHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRATATQAFFSITRAAPGARWGQQAH 60

Qy         61 SPLGTAADGHEVFYGIMFDAGSTGTRVHVFQFTRPPRETPTLTHETFKAVKPGLSAYADD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SPLGTAADGHEVFYGIMFDAGSTGTRVHVFQFTRPPRETPTLTHETFKAVKPGLSAYADD 120

Qy        121 VEKSAQGIRELLDVAKQDIPFDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASP 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VEKSAQGIRELLDVAKQDIPFDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASP 180

Qy        181 FLVGDDCVSIMNGTDEGVSAWITINFLTGSLKTPGGSSVGMLDLGGGSTQIAFLPRVEGT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 FLVGDDCVSIMNGTDEGVSAWITINFLTGSLKTPGGSSVGMLDLGGGSTQIAFLPRVEGT 240

Qy        241 LQASPPGYLTALRMFNRTYKLYSYSYLGLGLMSARLAILGGVEGQPAKDGKELVSPCLSP 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 LQASPPGYLTALRMFNRTYKLYSYSYLGLGLMSARLAILGGVEGQPAKDGKELVSPCLSP 300

Qy        301 SFKGEWEHAEVTYRVSGQKAAASLHELCAARVSEVLQNRVHRTEEVKHVDFYAFSYYYDL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 SFKGEWEHAEVTYRVSGQKAAASLHELCAARVSEVLQNRVHRTEEVKHVDFYAFSYYYDL 360

Qy        361 AAGVGLIDAEKGGSLVVGDFEIAAKYVCRTLETQPQSSPFSCMDLTYVSLLLQEFGFPRS 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db        361 AAGVGLIDAEKGGSLVVGDFEIAAKYVCRTLETQPQSSPFSCMDLTYVSLLLQEFGFPRS 420

Qy        421 KVLKLTRKIDNVETSWALGAIFHYIDSLNRQKSPAS 456
              |||||||||||||||||||||||||||||||||||
Db        421 KVLKLTRKIDNVETSWALGAIFHYIDSLNRQKSPAS 456


RESULT 2
US-09-908-510A-2
; Sequence 2, Application US/09908510A
; Patent No. 6759214
; GENERAL INFORMATION:
;  APPLICANT: Chadwick, Brian Paul
;  APPLICANT:  Frischauf, Anna Maria
;  TITLE OF INVENTION: METHODS AND  COMPOSITIONS RELATING TO CD39-LIKE POLYPEPTIDES AND
;  TITLE OF INVENTION:  ACIDS
;  FILE REFERENCE: 28110/36120E
;  CURRENT APPLICATION NUMBER: US/09/908,510A
;  CURRENT FILING DATE:  2001-07-13
;  PRIOR APPLICATION NUMBER: 09/240,639
;  PRIOR FILING DATE: 1999-01-29
;  NUMBER OF SEQ ID NOS: 32
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
;   LENGTH: 456
;   TYPE: PRT
;   ORGANISM: Homo Sapiens
US-09-908-510A-2

  Query Match            100.0%;  Score 2364;  DB 4;  Length 456;
  Best Local Similarity  100.0%;  Pred. No. 1.1e-230;
  Matches  456;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRKISNHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRATATQAFFSITRAAPGARWGQQAH 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRKISNHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRATATQAFFSITRAAPGARWGQQAH 60

Qy         61 SPLGTAADGHEVFYGIMFDAGSTGTRVHVFQFTRPPRETPTLTHETFKAVKPGLSAYADD 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SPLGTAADGHEVFYGIMFDAGSTGTRVHVFQFTRPPRETPTLTHETFKAVKPGLSAYADD 120

Qy        121 VEKSAQGIRELLDVAKQDIPFDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASP 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VEKSAQGIRELLDVAKQDIPFDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASP 180

Qy        181 FLVGDDCVSIMNGTDEGVSAWITINFLTGSLKTPGGSSVGMLDLGGGSTQIAFLPRVEGT 240
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 FLVGDDCVSIMNGTDEGVSAWITINFLTGSLKTPGGSSVGMLDLGGGSTQIAFLPRVEGT 240

Qy        241 LQASPPGYLTALRMFNRTYKLYSYSYLGLGLMSARLAILGGVEGQPAKDGKELVSPCLSP 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 LQASPPGYLTALRMFNRTYKLYSYSYLGLGLMSARLAILGGVEGQPAKDGKELVSPCLSP 300

Qy        301 SFKGEWEHAEVTYRVSGQKAAASLHELCAARVSEVLQNRVHRTEEVKHVDFYAFSYYYDL 360
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 SFKGEWEHAEVTYRVSGQKAAASLHELCAARVSEVLQNRVHRTEEVKHVDFYAFSYYYDL 360

Qy        361 AAGVGLIDAEKGGSLVVGDFEIAAKYVCRTLETQPQSSPFSCMDLTYVSLLLQEFGFPRS 420
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAGVGLIDAEKGGSLVVGDFEIAAKYVCRTLETQPQSSPFSCMDLTYVSLLLQEFGFPRS 420

Qy        421 KVLKLTRKIDNVETSWALGAIFHYIDSLNRQKSPAS 456
              |||||||||||||||||||||||||||||||||||
Db        421 KVLKLTRKIDNVETSWALGAIFHYIDSLNRQKSPAS 456


RESULT 3
US-09-905-744-2
; Sequence 2, Application US/09905744
; Patent No. 6780410
; GENERAL INFORMATION:
;  APPLICANT: Chadwick, Brian Paul
;  APPLICANT:  Frischauf, Anna-Maria
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE
;  TITLE OF INVENTION:  POLYPEPTIDES AND NUCLEIC ACIDS
;  FILE REFERENCE: 9598-066
;  CURRENT APPLICATION NUMBER: US/09/905,744
;  CURRENT FILING DATE:  2001-07-13
;  PRIOR APPLICATION NUMBER: 09/240,639
;  PRIOR FILING DATE: 1999-01-29
;  NUMBER OF SEQ ID NOS: 29
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 456
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-905-744-2

  Query Match            100.0%;  Score 2364;  DB 4;  Length 456;
  Best Local Similarity  100.0%;  Pred. No. 1.1e-230;
  Matches  456;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRKISNHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRATATQAFFSITRAAPGARWGQQAH 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRKISNHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRATATQAFFSITRAAPGARWGQQAH 60

Qy         61 SPLGTAADGHEVFYGIMFDAGSTGTRVHVFQFTRPPRETPTLTHETFKAVKPGLSAYADD 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SPLGTAADGHEVFYGIMFDAGSTGTRVHVFQFTRPPRETPTLTHETFKAVKPGLSAYADD 120

Qy        121 VEKSAQGIRELLDVAKQDIPFDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASP 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VEKSAQGIRELLDVAKQDIPFDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASP 180

Qy        181 FLVGDDCVSIMNGTDEGVSAWITINFLTGSLKTPGGSSVGMLDLGGGSTQIAFLPRVEGT 240
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 FLVGDDCVSIMNGTDEGVSAWITINFLTGSLKTPGGSSVGMLDLGGGSTQIAFLPRVEGT 240

Qy        241 LQASPPGYLTALRMFNRTYKLYSYSYLGLGLMSARLAILGGVEGQPAKDGKELVSPCLSP 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 LQASPPGYLTALRMFNRTYKLYSYSYLGLGLMSARLAILGGVEGQPAKDGKELVSPCLSP 300

Qy        301 SFKGEWEHAEVTYRVSGQKAAASLHELCAARVSEVLQNRVHRTEEVKHVDFYAFSYYYDL 360
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 SFKGEWEHAEVTYRVSGQKAAASLHELCAARVSEVLQNRVHRTEEVKHVDFYAFSYYYDL 360

Qy        361 AAGVGLIDAEKGGSLVVGDFEIAAKYVCRTLETQPQSSPFSCMDLTYVSLLLQEFGFPRS 420
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAGVGLIDAEKGGSLVVGDFEIAAKYVCRTLETQPQSSPFSCMDLTYVSLLLQEFGFPRS 420

Qy        421 KVLKLTRKIDNVETSWALGAIFHYIDSLNRQKSPAS 456
              |||||||||||||||||||||||||||||||||||
Db        421 KVLKLTRKIDNVETSWALGAIFHYIDSLNRQKSPAS 456


RESULT 4
US-10-107-660-2
; Sequence 2, Application US/10107660
; Patent No. 6780977
; GENERAL INFORMATION:
;  APPLICANT: Chadwick, Brian Paul
;  APPLICANT:  Frischauf, Anna-Maria
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE
;  TITLE OF INVENTION:  POLYPEPTIDES AND NUCLEIC ACIDS
;  FILE REFERENCE: 9598-066
;  CURRENT APPLICATION NUMBER: US/10/107,660
;  CURRENT FILING DATE:  2002-03-27
;  PRIOR APPLICATION NUMBER: US/09/240,639
;  PRIOR FILING DATE: 1998-01-29
;  NUMBER OF SEQ ID NOS: 29
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 456
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-107-660-2
```

```
  Query Match           100.0%;  Score 2364;  DB 4;  Length 456;
  Best Local Similarity  100.0%;  Pred. No. 1.1e-230;
  Matches  456;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRKISNHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRATATQAFFSITRAAPGARWGQQAH 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRKISNHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRATATQAFFSITRAAPGARWGQQAH 60

Qy         61 SPLGTAADGHEVFYGIMFDAGSTGTRVHVFQFTRPPRETPTLTHETFKAVKPGLSAYADD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SPLGTAADGHEVFYGIMFDAGSTGTRVHVFQFTRPPRETPTLTHETFKAVKPGLSAYADD 120

Qy        121 VEKSAQGIRELLDVAKQDIPFDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASP 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VEKSAQGIRELLDVAKQDIPFDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASP 180

Qy        181 FLVGDDCVSIMNGTDEGVSAWITINFLTGSLKTPGGSSVGMLDLGGGSTQIAFLPRVEGT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 FLVGDDCVSIMNGTDEGVSAWITINFLTGSLKTPGGSSVGMLDLGGGSTQIAFLPRVEGT 240

Qy        241 LQASPPGYLTALRMFNRTYKLYSYSYLGLGLMSARLAILGGVEGQPAKDGKELVSPCLSP 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 LQASPPGYLTALRMFNRTYKLYSYSYLGLGLMSARLAILGGVEGQPAKDGKELVSPCLSP 300

Qy        301 SFKGEWEHAEVTYRVSGQKAAASLHELCAARVSEVLQNRVHRTEEVKHVDFYAFSYYYDL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 SFKGEWEHAEVTYRVSGQKAAASLHELCAARVSEVLQNRVHRTEEVKHVDFYAFSYYYDL 360

Qy        361 AAGVGLIDAEKGGSLVVGDFEIAAKYVCRTLETQPQSSPFSCMDLTYVSLLLQEFGFPRS 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAGVGLIDAEKGGSLVVGDFEIAAKYVCRTLETQPQSSPFSCMDLTYVSLLLQEFGFPRS 420

Qy        421 KVLKLTRKIDNVETSWALGAIFHYIDSLNRQKSPAS 456
              ||||||||||||||||||||||||||||||||||||
Db        421 KVLKLTRKIDNVETSWALGAIFHYIDSLNRQKSPAS 456


RESULT 5
US-10-107-576-2
; Sequence 2, Application US/10107576
; Patent No. 6783959
; GENERAL INFORMATION:
;  APPLICANT: Chadwick, Brian Paul
;  APPLICANT:  Frischauf, Anna-Maria
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE
;  TITLE OF INVENTION:  POLYPEPTIDES AND NUCLEIC ACIDS
;  FILE REFERENCE: 9598-066
;  CURRENT APPLICATION NUMBER: US/10/107,576
;  CURRENT FILING DATE:  2002-03-27
;  PRIOR APPLICATION NUMBER: US/09/240,639
;  PRIOR FILING DATE: 1998-01-29
;  NUMBER OF SEQ ID NOS: 29
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 456
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-107-576-2

  Query Match           100.0%;  Score 2364;  DB 4;  Length 456;
  Best Local Similarity  100.0%;  Pred. No. 1.1e-230;
  Matches  456;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRKISNHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRATATQAFFSITRAAPGARWGQQAH 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRKISNHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRATATQAFFSITRAAPGARWGQQAH 60

Qy         61 SPLGTAADGHEVFYGIMFDAGSTGTRVHVFQFTRPPRETPTLTHETFKAVKPGLSAYADD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SPLGTAADGHEVFYGIMFDAGSTGTRVHVFQFTRPPRETPTLTHETFKAVKPGLSAYADD 120

Qy        121 VEKSAQGIRELLDVAKQDIPFDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASP 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VEKSAQGIRELLDVAKQDIPFDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASP 180

Qy        181 FLVGDDCVSIMNGTDEGVSAWITINFLTGSLKTPGGSSVGMLDLGGGSTQIAFLPRVEGT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 FLVGDDCVSIMNGTDEGVSAWITINFLTGSLKTPGGSSVGMLDLGGGSTQIAFLPRVEGT 240

Qy        241 LQASPPGYLTALRMFNRTYKLYSYSYLGLGLMSARLAILGGVEGQPAKDGKELVSPCLSP 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 LQASPPGYLTALRMFNRTYKLYSYSYLGLGLMSARLAILGGVEGQPAKDGKELVSPCLSP 300

Qy        301 SFKGEWEHAEVTYRVSGQKAAASLHELCAARVSEVLQNRVHRTEEVKHVDFYAFSYYYDL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 SFKGEWEHAEVTYRVSGQKAAASLHELCAARVSEVLQNRVHRTEEVKHVDFYAFSYYYDL 360

Qy        361 AAGVGLIDAEKGGSLVVGDFEIAAKYVCRTLETQPQSSPFSCMDLTYVSLLLQEFGFPRS 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAGVGLIDAEKGGSLVVGDFEIAAKYVCRTLETQPQSSPFSCMDLTYVSLLLQEFGFPRS 420

Qy        421 KVLKLTRKIDNVETSWALGAIFHYIDSLNRQKSPAS 456
              ||||||||||||||||||||||||||||||||||||
Db        421 KVLKLTRKIDNVETSWALGAIFHYIDSLNRQKSPAS 456


RESULT 6
US-09-905-732-2
; Sequence 2, Application US/09905732
; Patent No. 6787328
; GENERAL INFORMATION:
;  APPLICANT: Chadwick, Brian Paul
;  APPLICANT:  Frischauf, Anna-Maria
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE
;  TITLE OF INVENTION:  POLYPEPTIDES AND NUCLEIC ACIDS
;  FILE REFERENCE: 9598-066
;  CURRENT APPLICATION NUMBER: US/09/905,732
;  CURRENT FILING DATE:  2001-07-13
;  PRIOR APPLICATION NUMBER: US/09/240,639
;  PRIOR FILING DATE: 1998-01-29
;  NUMBER OF SEQ ID NOS: 29
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 456
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-905-732-2

  Query Match           100.0%;  Score 2364;  DB 4;  Length 456;
  Best Local Similarity  100.0%;  Pred. No. 1.1e-230;
  Matches  456;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRKISNHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRATATQAFFSITRAAPGARWGQQAH 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRKISNHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRATATQAFFSITRAAPGARWGQQAH 60

Qy         61 SPLGTAADGHEVFYGIMFDAGSTGTRVHVFQFTRPPRETPTLTHETFKAVKPGLSAYADD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SPLGTAADGHEVFYGIMFDAGSTGTRVHVFQFTRPPRETPTLTHETFKAVKPGLSAYADD 120

Qy        121 VEKSAQGIRELLDVAKQDIPFDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASP 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VEKSAQGIRELLDVAKQDIPFDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASP 180

Qy        181 FLVGDDCVSIMNGTDEGVSAWITINFLTGSLKTPGGSSVGMLDLGGGSTQIAFLPRVEGT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 FLVGDDCVSIMNGTDEGVSAWITINFLTGSLKTPGGSSVGMLDLGGGSTQIAFLPRVEGT 240

Qy        241 LQASPPGYLTALRMFNRTYKLYSYSYLGLGLMSARLAILGGVEGQPAKDGKELVSPCLSP 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 LQASPPGYLTALRMFNRTYKLYSYSYLGLGLMSARLAILGGVEGQPAKDGKELVSPCLSP 300

Qy        301 SFKGEWEHAEVTYRVSGQKAAASLHELCAARVSEVLQNRVHRTEEVKHVDFYAFSYYYDL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 SFKGEWEHAEVTYRVSGQKAAASLHELCAARVSEVLQNRVHRTEEVKHVDFYAFSYYYDL 360
```

```
Qy        361 AAGVGLIDAEKGGSLVVGDFEIAAKYVCRTLETQPQSSPFSCMDLTYVSLLLQEFGFPRS 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAGVGLIDAEKGGSLVVGDFEIAAKYVCRTLETQPQSSPFSCMDLTYVSLLLQEFGFPRS 420

Qy        421 KVLKLTRKIDNVETSWALGAIFHYIDSLNRQKSPAS 456
              |||||||||||||||||||||||||||||||||||||
Db        421 KVLKLTRKIDNVETSWALGAIFHYIDSLNRQKSPAS 456


RESULT 7
US-09-608-285A-27
; Sequence 27, Application US/09608285A
; Patent No. 6335013
; GENERAL INFORMATION:
;  APPLICANT:  Ford, John
;  APPLICANT:  Mulero, Julio
;  APPLICANT:  Yeung, George
;  TITLE OF INVENTION:  METHODS AND MATERIALS RELATING TO CD39-LIKE
;  TITLE OF INVENTION:  POLYPEPTIDES
;  FILE REFERENCE:  28110/36570
;  CURRENT APPLICATION NUMBER: US/09/608,285A
;  CURRENT FILING DATE:  2000-06-30
;  PRIOR APPLICATION NUMBER:  09/583,231
;  PRIOR FILING DATE:  2000-05-26
;  PRIOR APPLICATION NUMBER:  09/557,800
;  PRIOR FILING DATE:  2000-04-25
;  PRIOR APPLICATION NUMBER:  09/481,238
;  PRIOR FILING DATE:  2000-01-11
;  PRIOR APPLICATION NUMBER:  09/370,265
;  PRIOR FILING DATE:  1999-08-09
;  PRIOR APPLICATION NUMBER:  PCT/US99/16180
;  PRIOR FILING DATE:  1999-07-16
;  PRIOR APPLICATION NUMBER:  09/350,836
;  PRIOR FILING DATE:  1999-07-09
;  PRIOR APPLICATION NUMBER:  09/273,447
;  PRIOR FILING DATE:  1999-03-19
;  PRIOR APPLICATION NUMBER:  09/244,444
;  PRIOR FILING DATE:  1999-02-04
;  PRIOR APPLICATION NUMBER:  09/122,449
;  PRIOR FILING DATE:  1998-07-24
;  PRIOR APPLICATION NUMBER:  09/118,205
;  PRIOR FILING DATE:  1998-07-16
;  NUMBER OF SEQ ID NOS:  60
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 27
;   LENGTH: 484
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-608-285A-27

  Query Match           100.0%;  Score 2364;  DB 3;  Length 484;
  Best Local Similarity  100.0%;  Pred. No. 1.2e-230;
  Matches  456;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRKISNHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRATATQAFFSITRAAPGARWGQQAH 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         29 MRKISNHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRATATQAFFSITRAAPGARWGQQAH 88

Qy         61 SPLGTAADGHEVFYGIMFDAGSTGTRVHVFQFTRPPRETPTLTHETFKAVKPGLSAYADD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         89 SPLGTAADGHEVFYGIMFDAGSTGTRVHVFQFTRPPRETPTLTHETFKAVKPGLSAYADD 148

Qy        121 VEKSAQGIRELLDVAKQDIPFDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASP 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        149 VEKSAQGIRELLDVAKQDIPFDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASP 208

Qy        181 FLVGDDCVSIMNGTDEGVSAWITINFLTGSLKTPGGSSVGMLDLGGGSTQIAFLPRVEGT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        209 FLVGDDCVSIMNGTDEGVSAWITINFLTGSLKTPGGSSVGMLDLGGGSTQIAFLPRVEGT 268

Qy        241 LQASPPGYLTALRMFNRTYKLYSYSYLGLGLMSARLAILGGVEGQPAKDGKELVSPCLSP 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        269 LQASPPGYLTALRMFNRTYKLYSYSYLGLGLMSARLAILGGVEGQPAKDGKELVSPCLSP 328

Qy        301 SFKGEWEHAEVTYRVSGQKAAASLHELCAARVSEVLQNRVHRTEEVKHVDFYAFSYYYDL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        329 SFKGEWEHAEVTYRVSGQKAAASLHELCAARVSEVLQNRVHRTEEVKHVDFYAFSYYYDL 388

Qy        361 AAGVGLIDAEKGGSLVVGDFEIAAKYVCRTLETQPQSSPFSCMDLTYVSLLLQEFGFPRS 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        389 AAGVGLIDAEKGGSLVVGDFEIAAKYVCRTLETQPQSSPFSCMDLTYVSLLLQEFGFPRS 448

Qy        421 KVLKLTRKIDNVETSWALGAIFHYIDSLNRQKSPAS 456
              |||||||||||||||||||||||||||||||||||||
Db        449 KVLKLTRKIDNVETSWALGAIFHYIDSLNRQKSPAS 484


RESULT 8
US-09-370-265-27
; Sequence 27, Application US/09370265
; Patent No. 6447771
; GENERAL INFORMATION:
;  APPLICANT: Ford, John
;  APPLICANT: Mulero, Julio
;  TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE
;  TITLE OF INVENTION: POLYPEPTIDES
;  FILE REFERENCE: 28111/35908
;  CURRENT APPLICATION NUMBER: US/09/370,265
;  CURRENT FILING DATE: 1999-08-09
;  EARLIER APPLICATION NUMBER: PCT/US99/16180
;  EARLIER FILING DATE: 1999-07-16
;  EARLIER APPLICATION NUMBER: 09/350,836
;  EARLIER FILING DATE: 1999-07-09
;  EARLIER APPLICATION NUMBER: 09/273,447
;  EARLIER FILING DATE: 1999-03-19
;  EARLIER APPLICATION NUMBER: 09/244,444
;  EARLIER FILING DATE: 1999-02-04
;  EARLIER APPLICATION NUMBER: 09/122,449
;  EARLIER FILING DATE: 1998-07-24
;  EARLIER APPLICATION NUMBER: 09/118,205
;  EARLIER FILING DATE: 1998-07-16
;  NUMBER OF SEQ ID NOS: 37
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 27
;   LENGTH: 484
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-370-265-27

  Query Match           100.0%;  Score 2364;  DB 4;  Length 484;
  Best Local Similarity  100.0%;  Pred. No. 1.2e-230;
  Matches  456;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRKISNHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRATATQAFFSITRAAPGARWGQQAH 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         29 MRKISNHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRATATQAFFSITRAAPGARWGQQAH 88

Qy         61 SPLGTAADGHEVFYGIMFDAGSTGTRVHVFQFTRPPRETPTLTHETFKAVKPGLSAYADD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         89 SPLGTAADGHEVFYGIMFDAGSTGTRVHVFQFTRPPRETPTLTHETFKAVKPGLSAYADD 148

Qy        121 VEKSAQGIRELLDVAKQDIPFDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASP 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        149 VEKSAQGIRELLDVAKQDIPFDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASP 208

Qy        181 FLVGDDCVSIMNGTDEGVSAWITINFLTGSLKTPGGSSVGMLDLGGGSTQIAFLPRVEGT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        209 FLVGDDCVSIMNGTDEGVSAWITINFLTGSLKTPGGSSVGMLDLGGGSTQIAFLPRVEGT 268

Qy        241 LQASPPGYLTALRMFNRTYKLYSYSYLGLGLMSARLAILGGVEGQPAKDGKELVSPCLSP 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        269 LQASPPGYLTALRMFNRTYKLYSYSYLGLGLMSARLAILGGVEGQPAKDGKELVSPCLSP 328

Qy        301 SFKGEWEHAEVTYRVSGQKAAASLHELCAARVSEVLQNRVHRTEEVKHVDFYAFSYYYDL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db        329 SFKGEWEHAEVTYRVSGQKAAASLHELCAARVSEVLQNRVHRTEEVKHVDFYAFSYYYDL 388

Qy        361 AAGVGLIDAEKGGSLVVGDFEIAAKYVCRTLETQPQSSPFSCMDLTYVSLLLQEFGFPRS 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        389 AAGVGLIDAEKGGSLVVGDFEIAAKYVCRTLETQPQSSPFSCMDLTYVSLLLQEFGFPRS 448

Qy        421 KVLKLTRKIDNVETSWALGAIFHYIDSLNRQKSPAS 456
              ||||||||||||||||||||||||||||||||||||
Db        449 KVLKLTRKIDNVETSWALGAIFHYIDSLNRQKSPAS 484


RESULT 9
US-09-557-800C-27
; Sequence 27, Application US/09557800C
; Patent No. 6476211
; GENERAL INFORMATION:
;  APPLICANT: Ford, John
;  APPLICANT:  Mulero, Julio
;  APPLICANT:  Yeung, George
;  TITLE OF INVENTION: Methods and Materials Relating to CD39-Like
;  TITLE OF INVENTION:  Polypeptides
;  FILE REFERENCE: 28110/36457
;  CURRENT APPLICATION NUMBER: US/09/557,800C
;  CURRENT FILING DATE:  2000-04-25
;  PRIOR APPLICATION NUMBER: 09/481,238
;  PRIOR FILING DATE: 2000-01-11
;  PRIOR APPLICATION NUMBER: 09/370,265
;  PRIOR FILING DATE: 1999-08-09
;  PRIOR APPLICATION NUMBER: PCT/US99/16180
;  PRIOR FILING DATE: 1999-07-16
;  PRIOR APPLICATION NUMBER: 09/350836
;  PRIOR FILING DATE: 1999-07-09
;  PRIOR APPLICATION NUMBER: 09/273447
;  PRIOR FILING DATE: 1999-03-19
;  PRIOR APPLICATION NUMBER: 09/122449
;  PRIOR FILING DATE: 1998-07-24
;  PRIOR APPLICATION NUMBER: 09/244444
;  PRIOR FILING DATE: 1999-02-04
;  PRIOR APPLICATION NUMBER: 09/118,205
;  PRIOR FILING DATE: 1998-07-16
;  NUMBER OF SEQ ID NOS: 56
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 27
;   LENGTH: 484
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-557-800C-27

  Query Match           100.0%;  Score 2364;  DB 4;  Length 484;
  Best Local Similarity  100.0%;  Pred. No. 1.2e-230;
  Matches  456;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRKISNHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRATATQAFFSITRAAPGARWGQQAH 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         29 MRKISNHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRATATQAFFSITRAAPGARWGQQAH 88

Qy         61 SPLGTAADGHEVFYGIMFDAGSTGTRVHVFQFTRPPRETPTLTHETFKAVKPGLSAYADD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         89 SPLGTAADGHEVFYGIMFDAGSTGTRVHVFQFTRPPRETPTLTHETFKAVKPGLSAYADD 148

Qy        121 VEKSAQGIRELLDVAKQDIPFDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASP 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        149 VEKSAQGIRELLDVAKQDIPFDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASP 208

Qy        181 FLVGDDCVSIMNGTDEGVSAWITINFLTGSLKTPGGSSVGMLDLGGGSTQIAFLPRVEGT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        209 FLVGDDCVSIMNGTDEGVSAWITINFLTGSLKTPGGSSVGMLDLGGGSTQIAFLPRVEGT 268

Qy        241 LQASPPGYLTALRMFNRTYKLYSYSYLGLGLMSARLAILGGVEGQPAKDGKELVSPCLSP 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        269 LQASPPGYLTALRMFNRTYKLYSYSYLGLGLMSARLAILGGVEGQPAKDGKELVSPCLSP 328

Qy        301 SFKGEWEHAEVTYRVSGQKAAASLHELCAARVSEVLQNRVHRTEEVKHVDFYAFSYYYDL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        329 SFKGEWEHAEVTYRVSGQKAAASLHELCAARVSEVLQNRVHRTEEVKHVDFYAFSYYYDL 388

Qy        361 AAGVGLIDAEKGGSLVVGDFEIAAKYVCRTLETQPQSSPFSCMDLTYVSLLLQEFGFPRS 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        389 AAGVGLIDAEKGGSLVVGDFEIAAKYVCRTLETQPQSSPFSCMDLTYVSLLLQEFGFPRS 448

Qy        421 KVLKLTRKIDNVETSWALGAIFHYIDSLNRQKSPAS 456
              ||||||||||||||||||||||||||||||||||||
Db        449 KVLKLTRKIDNVETSWALGAIFHYIDSLNRQKSPAS 484


RESULT 10
US-09-370-625A-27
; Sequence 27, Application US/09370625A
; Patent No. 6600032
; GENERAL INFORMATION:
;  APPLICANT: Ford, John
;  APPLICANT:  Mulero, Julio
;  TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE POLYPEPTIDES
;  FILE REFERENCE: 28110/35908
;  CURRENT APPLICATION NUMBER: US/09/370,625A
;  CURRENT FILING DATE:  1999-08-09
;  PRIOR APPLICATION NUMBER: PCT/US99/16180
;  PRIOR FILING DATE: 1999-07-16
;  PRIOR APPLICATION NUMBER: 09/350,836
;  PRIOR FILING DATE: 1999-07-09
;  PRIOR APPLICATION NUMBER: 09/273,447
;  PRIOR FILING DATE: 1999-03-19
;  NUMBER OF SEQ ID NOS: 39
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 27
;   LENGTH: 484
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-370-625A-27

  Query Match           100.0%;  Score 2364;  DB 4;  Length 484;
  Best Local Similarity  100.0%;  Pred. No. 1.2e-230;
  Matches  456;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRKISNHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRATATQAFFSITRAAPGARWGQQAH 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         29 MRKISNHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRATATQAFFSITRAAPGARWGQQAH 88

Qy         61 SPLGTAADGHEVFYGIMFDAGSTGTRVHVFQFTRPPRETPTLTHETFKAVKPGLSAYADD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         89 SPLGTAADGHEVFYGIMFDAGSTGTRVHVFQFTRPPRETPTLTHETFKAVKPGLSAYADD 148

Qy        121 VEKSAQGIRELLDVAKQDIPFDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASP 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        149 VEKSAQGIRELLDVAKQDIPFDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASP 208

Qy        181 FLVGDDCVSIMNGTDEGVSAWITINFLTGSLKTPGGSSVGMLDLGGGSTQIAFLPRVEGT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        209 FLVGDDCVSIMNGTDEGVSAWITINFLTGSLKTPGGSSVGMLDLGGGSTQIAFLPRVEGT 268

Qy        241 LQASPPGYLTALRMFNRTYKLYSYSYLGLGLMSARLAILGGVEGQPAKDGKELVSPCLSP 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        269 LQASPPGYLTALRMFNRTYKLYSYSYLGLGLMSARLAILGGVEGQPAKDGKELVSPCLSP 328

Qy        301 SFKGEWEHAEVTYRVSGQKAAASLHELCAARVSEVLQNRVHRTEEVKHVDFYAFSYYYDL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        329 SFKGEWEHAEVTYRVSGQKAAASLHELCAARVSEVLQNRVHRTEEVKHVDFYAFSYYYDL 388

Qy        361 AAGVGLIDAEKGGSLVVGDFEIAAKYVCRTLETQPQSSPFSCMDLTYVSLLLQEFGFPRS 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        389 AAGVGLIDAEKGGSLVVGDFEIAAKYVCRTLETQPQSSPFSCMDLTYVSLLLQEFGFPRS 448

Qy        421 KVLKLTRKIDNVETSWALGAIFHYIDSLNRQKSPAS 456
              ||||||||||||||||||||||||||||||||||||
Db        449 KVLKLTRKIDNVETSWALGAIFHYIDSLNRQKSPAS 484
```

```
RESULT 11
US-09-608-285A-60
; Sequence 60, Application US/09608285A
; Patent No. 6335013
; GENERAL INFORMATION:
;  APPLICANT:  Ford, John
;  APPLICANT:  Mulero, Julio
;  APPLICANT:  Yeung, George
;  TITLE OF INVENTION:  METHODS AND MATERIALS RELATING TO CD39-LIKE
;  TITLE OF INVENTION:  POLYPEPTIDES
;  FILE REFERENCE:  28110/36570
;  CURRENT APPLICATION NUMBER: US/09/608,285A
;  CURRENT FILING DATE:  2000-06-30
;  PRIOR APPLICATION NUMBER:  09/583,231
;  PRIOR FILING DATE:  2000-05-26
;  PRIOR APPLICATION NUMBER:  09/557,800
;  PRIOR FILING DATE:  2000-04-25
;  PRIOR APPLICATION NUMBER:  09/481,238
;  PRIOR FILING DATE:  2000-01-11
;  PRIOR APPLICATION NUMBER:  09/370,265
;  PRIOR FILING DATE:  1999-08-09
;  PRIOR APPLICATION NUMBER:  PCT/US99/16180
;  PRIOR FILING DATE:  1999-07-16
;  PRIOR APPLICATION NUMBER:  09/350,836
;  PRIOR FILING DATE:  1999-07-09
;  PRIOR APPLICATION NUMBER:  09/273,447
;  PRIOR FILING DATE:  1999-03-19
;  PRIOR APPLICATION NUMBER:  09/244,444
;  PRIOR FILING DATE:  1999-02-04
;  PRIOR APPLICATION NUMBER:  09/122,449
;  PRIOR FILING DATE:  1998-07-24
;  PRIOR APPLICATION NUMBER:  09/118,205
;  PRIOR FILING DATE:  1998-07-16
;  NUMBER OF SEQ ID NOS:  60
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 60
;   LENGTH: 471
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-608-285A-60

  Query Match             84.7%;  Score 2003;  DB 3;  Length 471;
  Best Local Similarity   98.5%;  Pred. No. 4.6e-194;
  Matches  388;  Conservative    1;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 MRKISNHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRATATQAFFSITRAAPGARWGQQAH 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         29 MRKISNHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRATATQAFFSITRAAPGARWGQQAH 88

Qy         61 SPLGTAADGHEVFYGIMFDAGSTGTRVHVFQFTRPPRETPTLTHETFKAVKPGLSAYADD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         89 SPLGTAADGHEVFYGIMFDAGSTGTRVHVFQFTRPPRETPTLTHETFKAVKPGLSAYADD 148

Qy        121 VEKSAQGIRELLDVAKQDIPFDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASP 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        149 VEKSAQGIRELLDVAKQDIPFDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASP 208

Qy        181 FLVGDDCVSIMNGTDEGVSAWITINFLTGSLKTPGGSSVGMLDLGGGSTQIAFLPRVEGT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        209 FLVGDDCVSIMNGTDEGVSAWITINFLTGSLKTPGGSSVGMLDLGGGSTQIAFLPRVEGT 268

Qy        241 LQASPPGYLTALRMFNRTYKLYSYSYLGLGLMSARLAILGGVEGQPAKDGKELVSPCLSP 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        269 LQASPPGYLTALRMFNRTYKLYSYSYLGLGLMSARLAILGGVEGQPAKDGKELVSPCLSP 328

Qy        301 SFKGEWEHAEVTYRVSGQKAAASLHELCAARVSEVLQNRVHRTEEVKHVDFYAFSYYYDL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        329 SFKGEWEHAEVTYRVSGQKAAASLHELCAARVSEVLQNRVHRTEEVKHVDFYAFSYYYDL 388

Qy        361 AAGVGLIDAEKGGSLVVGDFEIAAKYVCRTLETQ 394
              ||||||||||||||||||||||||||||||||||| :
Db        389 AAGVGLIDAEKGGSLVVGDFEIAAKYGGSHLERE 422
```

```
RESULT 12
US-09-608-285A-3
; Sequence 3, Application US/09608285A
; Patent No. 6335013
; GENERAL INFORMATION:
;  APPLICANT:  Ford, John
;  APPLICANT:  Mulero, Julio
;  APPLICANT:  Yeung, George
;  TITLE OF INVENTION:  METHODS AND MATERIALS RELATING TO CD39-LIKE
;  TITLE OF INVENTION:  POLYPEPTIDES
;  FILE REFERENCE:  28110/36570
;  CURRENT APPLICATION NUMBER: US/09/608,285A
;  CURRENT FILING DATE:  2000-06-30
;  PRIOR APPLICATION NUMBER:  09/583,231
;  PRIOR FILING DATE:  2000-05-26
;  PRIOR APPLICATION NUMBER:  09/557,800
;  PRIOR FILING DATE:  2000-04-25
;  PRIOR APPLICATION NUMBER:  09/481,238
;  PRIOR FILING DATE:  2000-01-11
;  PRIOR APPLICATION NUMBER:  09/370,265
;  PRIOR FILING DATE:  1999-08-09
;  PRIOR APPLICATION NUMBER:  PCT/US99/16180
;  PRIOR FILING DATE:  1999-07-16
;  PRIOR APPLICATION NUMBER:  09/350,836
;  PRIOR FILING DATE:  1999-07-09
;  PRIOR APPLICATION NUMBER:  09/273,447
;  PRIOR FILING DATE:  1999-03-19
;  PRIOR APPLICATION NUMBER:  09/244,444
;  PRIOR FILING DATE:  1999-02-04
;  PRIOR APPLICATION NUMBER:  09/122,449
;  PRIOR FILING DATE:  1998-07-24
;  PRIOR APPLICATION NUMBER:  09/118,205
;  PRIOR FILING DATE:  1998-07-16
;  NUMBER OF SEQ ID NOS:  60
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 3
;   LENGTH: 428
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-608-285A-3

  Query Match             42.3%;  Score 999;  DB 3;  Length 428;
  Best Local Similarity   52.4%;  Pred. No. 2.2e-92;
  Matches  204;  Conservative   56;  Mismatches  123;  Indels    6;  Gaps    4;

Qy         62 PLGTAADGHEVFYGIMFDAGSTGTRVHVFQFT-RPPRETPTLTHETFKAVKPGLSAYADD 120
              |:  :|       |||||||||||||||:||:  |  :  |  :  |  |   |  |:|||||||: |
Db         40 PINVSA---STLYGIMFDAGSTGTRIHVYTFVQKMPGQLPILEGEVFDSVKPGLSAFVDQ 96

Qy        121 VEKSAQGIRELLDVAKQDIPFDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASP 180
              ::  |: ::  ||:|||   ||    || ||:|||||||||||||   ||: || :|||:|: ||
Db         97 PKQGAETVQGLLEVAKDSIPRSHWKKTPVVLKATAGLRLLPEHKAKALLFEVKEIFRKSP 156

Qy        181 FLVGDDCVSIMNGTDEGVSAWITINFLTGSLKTPGGSSVGMLDLGGGSTQIAFLPRVEGT 240
              |||    ||||:|:|||: ||:|:|||||  |      :|| |||||  |||| |||: | |
Db        157 FLVPKGSVSIMDGSDEGILAWVTVNFLTGQLHGHRQETVGTLDLGGASTQITFLPQFEKT 216

Qy        241 LQASPPGYLTALRMFNRTYKLYSYSYLGLGLMSARLAILGGVEGQPAKDGKELVSPCLSP 300
              |: :| ||||:  ||| |||||::|||| || :|||| || :|  :   ||    | ||
Db        217 LEQTPRGYLTSFEMFNSTYKLYTHSYLGFGLKAARLATLGALETE-GTDGHTFRSACLPR 275

Qy        301 SFKGEWEHAEVTYRVSGQKAAASLHELCAARVSEVLQNRVHRTEEVKHVDFYAFSYYYDL 360
              : ||    | |:  | :       | | | |  |:: ::|: |||:   |||||||||
Db        276 WLEAEWIFGGVKYQYGGNQEGEVGFEPCYAEVLRVVRGKLHQPEEVQRGSFYAFSYYYDR 335

Qy        361 AAGVGLIDAEKGGSLVVGDFEIAAKYVCRTLETQPQSSPFSCMDLTYVSLLLQE-FGFPR 419
              |    :|| |||| | | |||  |: ||  ||     ||| ||||:|:: ||:: |||
Db        336 AVDTDMIDYEKGGILKVEDFERKAREVCDNLENFTSGSPFLCMDLSYITALLKDGFGFAD 395

Qy        420 SKVLKLTRKIDNVETSWALGAIFHYIDSL 448
              | ||:||:|::|:|| ||||| || : ||
```

```
Db        396 STVLQLTKKVNNIETGWALGATFHLLQSL 424


RESULT 13
US-09-608-285A-5
; Sequence 5, Application US/09608285A
; Patent No. 6335013
; GENERAL INFORMATION:
;  APPLICANT:  Ford, John
;  APPLICANT:  Mulero, Julio
;  APPLICANT:  Yeung, George
;  TITLE OF INVENTION:  METHODS AND MATERIALS RELATING TO CD39-LIKE
;  TITLE OF INVENTION:  POLYPEPTIDES
;  FILE REFERENCE:  28110/36570
;  CURRENT APPLICATION NUMBER: US/09/608,285A
;  CURRENT FILING DATE:  2000-06-30
;  PRIOR APPLICATION NUMBER:  09/583,231
;  PRIOR FILING DATE:  2000-05-26
;  PRIOR APPLICATION NUMBER:  09/557,800
;  PRIOR FILING DATE:  2000-04-25
;  PRIOR APPLICATION NUMBER:  09/481,238
;  PRIOR FILING DATE:  2000-01-11
;  PRIOR APPLICATION NUMBER:  09/370,265
;  PRIOR FILING DATE:  1999-08-09
;  PRIOR APPLICATION NUMBER:  PCT/US99/16180
;  PRIOR FILING DATE:  1999-07-16
;  PRIOR APPLICATION NUMBER:  09/350,836
;  PRIOR FILING DATE:  1999-07-09
;  PRIOR APPLICATION NUMBER:  09/273,447
;  PRIOR FILING DATE:  1999-03-19
;  PRIOR APPLICATION NUMBER:  09/244,444
;  PRIOR FILING DATE:  1999-02-04
;  PRIOR APPLICATION NUMBER:  09/122,449
;  PRIOR FILING DATE:  1998-07-24
;  PRIOR APPLICATION NUMBER:  09/118,205
;  PRIOR FILING DATE:  1998-07-16
;  NUMBER OF SEQ ID NOS:  60
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 5
;   LENGTH: 428
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-608-285A-5

  Query Match           42.3%;  Score 999;  DB 3;  Length 428;
  Best Local Similarity  52.4%;  Pred. No. 2.2e-92;
  Matches  204;  Conservative   56;  Mismatches  123;  Indels    6;  Gaps    4;

Qy         62 PLGTAADGHEVFYGIMFDAGSTGTRVHVFQFT-RPPRETPTLTHETFKAVKPGLSAYADD 120
              |:  :|      |||||||||||||:||: |  : | : | |  | | :|||||||: |
Db         40 PINVSA---STLYGIMFDAGSTGTRIHVYTFVQKMPGQLPILEGEVFDSVKPGLSAFVDQ 96

Qy        121 VEKSAQGIRELLDVAKQDIPFDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASP 180
               :: |: :: ||:|||  ||   || ||:||||||||||||  ||: || :|||:|: ||
Db         97 PKQGAETVQGLLEVAKDSIPRSHWKKTPVVLKATAGLRLLPEHKAKALLFEVKEIFRKSP 156

Qy        181 FLVGDDCVSIMNGTDEGVSAWITINFLTGSLKTPGGSSVGMLDLGGGSTQIAFLPRVEGT 240
              |||    ||||:|:|||: ||:|:|||||  |      :|| ||||| |||| |||: | |
Db        157 FLVPKGSVSIMDGSDEGILAWVTVNFLTGQLHGHRQETVGTLDLGGASTQITFLPQFEKT 216

Qy        241 LQASPPGYLTALRMFNRTYKLYSYSYLGLGLMSARLAILGGVEGQPAKDGKELVSPCLSP 300
              |: :| ||||:  ||| ||||||::|||| || :|||| || :| :   ||    | ||
Db        217 LEQTPRGYLTSFEMFNSTYKLYTHSYLGFGLKAARLATLGALETE-GTDGHTFRSACLPR 275

Qy        301 SFKGEWEHAEVTYRVSGQKAAASLHELCAARVSEVLQNRVHRTEEVKHVDFYAFSYYYDL 360
              : ||    | |:  | :       | | | |  |:: ::|: |||:   |||||||||
Db        276 WLEAEWIFGGVKYQYGGNQEGEVGFEPCYAEVLRVVRGKLHQPEEVQRGSFYAFSYYYDR 335

Qy        361 AAGVGLIDAEKGGSLVVGDFEIAAKYVCRTLETQPQSSPFSCMDLTYVSLLLQE-FGFPR 419
              |    :|| |||| | | |||  |: ||  ||     ||| |||:|:: ||:: |||
Db        336 AVDTDMIDYEKGGILKVEDFERKAREVCDNLENFTSGSPFLCMDLSYITALLKDGFGFAD 395

Qy        420 SKVLKLTRKIDNVETSWALGAIFHYIDSL 448
              | ||:||:|::|:|| ||||| || : ||
Db        396 STVLQLTKKVNNIETGWALGATFHLLQSL 424


RESULT 14
US-09-240-639-6
; Sequence 6, Application US/09240639
; Patent No. 6350447
; GENERAL INFORMATION:
;  APPLICANT: Chadwick, Brian Paul
;  APPLICANT: Frischauf, Anna-Maria
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE
;  TITLE OF INVENTION: POLYPEPTIDES AND NUCLEIC ACIDS
;  FILE REFERENCE: 9598-066
;  CURRENT APPLICATION NUMBER: US/09/240,639
;  CURRENT FILING DATE: 1998-01-29
;  NUMBER OF SEQ ID NOS: 29
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
;   LENGTH: 428
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-240-639-6

  Query Match           42.3%;  Score 999;  DB 3;  Length 428;
  Best Local Similarity  52.4%;  Pred. No. 2.2e-92;
  Matches  204;  Conservative   56;  Mismatches  123;  Indels    6;  Gaps    4;

Qy         62 PLGTAADGHEVFYGIMFDAGSTGTRVHVFQFT-RPPRETPTLTHETFKAVKPGLSAYADD 120
              |:  :|      |||||||||||||:||: |  : | : | |  | | :|||||||: |
Db         40 PINVSA---STLYGIMFDAGSTGTRIHVYTFVQKMPGQLPILEGEVFDSVKPGLSAFVDQ 96

Qy        121 VEKSAQGIRELLDVAKQDIPFDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASP 180
               :: |: :: ||:|||  ||   || ||:||||||||||||  ||: || :|||:|: ||
Db         97 PKQGAETVQGLLEVAKDSIPRSHWKKTPVVLKATAGLRLLPEHKAKALLFEVKEIFRKSP 156

Qy        181 FLVGDDCVSIMNGTDEGVSAWITINFLTGSLKTPGGSSVGMLDLGGGSTQIAFLPRVEGT 240
              |||    ||||:|:|||: ||:|:|||||  |      :|| ||||| |||| |||: | |
Db        157 FLVPKGSVSIMDGSDEGILAWVTVNFLTGQLHGHRQETVGTLDLGGASTQITFLPQFEKT 216

Qy        241 LQASPPGYLTALRMFNRTYKLYSYSYLGLGLMSARLAILGGVEGQPAKDGKELVSPCLSP 300
              |: :| ||||:  ||| ||||||::|||| || :|||| || :| :   ||    | ||
Db        217 LEQTPRGYLTSFEMFNSTYKLYTHSYLGFGLKAARLATLGALETE-GTDGHTFRSACLPR 275

Qy        301 SFKGEWEHAEVTYRVSGQKAAASLHELCAARVSEVLQNRVHRTEEVKHVDFYAFSYYYDL 360
              : ||    | |:  | :       | | | |  |:: ::|: |||:   |||||||||
Db        276 WLEAEWIFGGVKYQYGGNQEGEVGFEPCYAEVLRVVRGKLHQPEEVQRGSFYAFSYYYDR 335

Qy        361 AAGVGLIDAEKGGSLVVGDFEIAAKYVCRTLETQPQSSPFSCMDLTYVSLLLQE-FGFPR 419
              |    :|| |||| | | |||  |: ||  ||     ||| |||:|:: ||:: |||
Db        336 AVDTDMIDYEKGGILKVEDFERKAREVCDNLENFTSGSPFLCMDLSYITALLKDGFGFAD 395

Qy        420 SKVLKLTRKIDNVETSWALGAIFHYIDSL 448
              | ||:||:|::|:|| ||||| || : ||
Db        396 STVLQLTKKVNNIETGWALGATFHLLQSL 424


RESULT 15
US-09-240-639-9
; Sequence 9, Application US/09240639
; Patent No. 6350447
; GENERAL INFORMATION:
;  APPLICANT: Chadwick, Brian Paul
;  APPLICANT: Frischauf, Anna-Maria
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE
;  TITLE OF INVENTION: POLYPEPTIDES AND NUCLEIC ACIDS
;  FILE REFERENCE: 9598-066
;  CURRENT APPLICATION NUMBER: US/09/240,639
;  CURRENT FILING DATE: 1998-01-29
;  NUMBER OF SEQ ID NOS: 29
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
;   LENGTH: 428
```

; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-240-639-9

Query Match 42.3%; Score 999; DB 3; Length 428;
Best Local Similarity 52.4%; Pred. No. 2.2e-92;
Matches 204; Conservative 56; Mismatches 123; Indels 6; Gaps 4;

```
Qy          62 PLGTAADGHEVFYGIMFDAGSTGTRVHVFQFT-RPPRETPTLTHETFKAVKPGLSAYADD 120
               |:  :|      ||||||||||||:||: |  : | : | |  | | :|||||||: |
Db          40 PINVSA---STLYGIMFDAGSTGTRIHVYTFVQKMPGQLPILEGEVFDSVKPGLSAFVDQ 96

Qy         121 VEKSAQGIRELLDVAKQDIPFDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASP 180
                :: |: :: ||:|||  ||   || ||:||||||||||||  ||: || :|||:|: ||
Db          97 PKQGAETVQGLLEVAKDSIPRSHWKKTPVVLKATAGLRLLPEHKAKALLFEVKEIFRKSP 156

Qy         181 FLVGDDCVSIMNGTDEGVSAWITINFLTGSLKTPGGSSVGMLDLGGGSTQIAFLPRVEGT 240
               |||    ||||:|:|||: ||:|:|||| |      :|| ||||| |||| |||: | |
Db         157 FLVPKGSVSIMDGSDEGILAWVTVNFLTGQLHGHRQETVGTLDLGGASTQITFLPQFEKT 216

Qy         241 LQASPPGYLTALRMFNRTYKLYSYSYLGLGLMSARLAILGGVEGQPAKDGKELVSPCLSP 300
               |: :| ||||:  ||| ||||::|||| || :|||| || :| :   ||    | ||
Db         217 LEQTPRGYLTSFEMFNSTYKLYTHSYLGFGLKAARLATLGALETE-GTDGHTFRSACLPR 275

Qy         301 SFKGEWEHAEVTYRVSGQKAAASLHELCAARVSEVLQNRVHRTEEVKHVDFYAFSYYYDL 360
              : ||    | |:  | :      | | | |  |:: ::|: |||:   |||||||||
Db         276 WLEAEWIFGGVKYQYGGNQEGEVGFEPCYAEVLRVVRGKLHQPEEVQRGSFYAFSYYYDR 335

Qy         361 AAGVGLIDAEKGGSLVVGDFEIAAKYVCRTLETQPQSSPFSCMDLTYVSLLLQE-FGFPR 419
               |    :|| |||| | | |||  |: ||  ||    ||| ||||:|:: ||:: |||
Db         336 AVDTDMIDYEKGGILKVEDFERKAREVCDNLENFTSGSPFLCMDLSYITALLKDGFGFAD 395

Qy         420 SKVLKLTRKIDNVETSWALGAIFHYIDSL 448
               | ||:||:|::|:|| ||||| || : ||
Db         396 STVLQLTKKVNNIETGWALGATFHLLQSL 424
```

Search completed: November 16, 2004, 17:01:10
Job time : 42 secs